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crystal crystal

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Title: Perfect score:

Sequence:

Scoring table:

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A; MCGCULE type: DNA
A; Residues: 1-1180 < WARN-
A; Residues: 1-1180 < WARN-
A; Residues: 1-1180 < WARN-
A; Cross-references: UNIPROT: P16480; UNIPARC: UP1000016EA42; GB: Y00423; NID: 940351; PIDN: CA; Cross-references: UNIPROT: P16480; UNIPARC: UP1000012; NID: 940351; PIDN: CA; Nishimoto, T.; Yoshisue, H.; Ihara, K.; Sakai, H.; Komano, T.
R; Nishimoto, T.; Yoshisue, H.; Ihara, K.; Sakai, H.; Komano, T.
A; Title: Punctional analysis of block 5, one of the highly conserved amino acid sequence A; Reference number: 848691; MUID: 94307434; PMID: 7913448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          paragporal crystal protein cry4hal - Bacillus thuringiensis subsp. israelensis
N;Alternate names: parasporal crystal protein cryIVA
C;Species: Bacillus thuringdensis subsp. israelensis
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 05-Oct-2004
C;Accession: A26858; S48691
R;Ward, E.S.; Ellar, D.J.
R;Ward, E.S.; Ellar, D.J.
A;Title: Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene encoding A;Reference number: A26858; MUID:88015571; PMID:2821500
                                                                parasporal crystal parasporal crystal
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Matches:
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A; Molecule type: DNA
A; Residues: 667-676 < NIS>
A; Cross-references: UNIPARC:UP1000017819A
C; Superfamily: Parasporal crystal protein
C; Keywords: delta-endotoxin
S11446
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-MODEL=frame+ n2p.model -DEV-xlp
-Q=/CGM2 1/USFTO spool p/USION082570/runat 12012006 060222 7522/app query.fasta_1.2375
-Q=/CGM2 1/USFTO spool p/USION082570/runat 12012006 060222 7522/app query.fasta_1.2375
-DB=FIR -QFWT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNITS=bits -START=1 -RND=-1 -MATRIX=bitonum62 -TRANS=biuman40.cdi -LIST=45
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-UNITS=bits -START=1 -NORM==AR -HRABEIX==500 -MINLEN=0 -MAXLEN=2000000000
-USER-USION082570 @CGN 1 1 57 @runat 12012006 060222 7522 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-NOWMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV TIMBOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBILOP=6 -DBIEXT=7
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(c) 1993 - 2006 Compugen Ltd
                                                                                                                       OM nucleic - protein search, using frame_plus_n2p model
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Result Š.

44 TyrLysAspTrpLeuAsnValCysGlnAspAsnGlnGlnTyrGlyAsnAsnAsnAsnCGGTACTG 53  193 TTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATTGTATCGGTACTCTG 252  193 TTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATTGTATCGGTACTCTG 252  64 PheAlaSerSerGluThrIleValGlyValSerAlaGlyIleIleValValGlyThrMet 83  253 TTAGCCGGTATAGGTGGGCTCCTTCTATATCCGGACCGATAGGTGCTATA 312	ADATATICTTTTGGTACCCTAATCACTGTCTTTTGGCCCGCGCAAAACAAGACAAAACA 37	GTATGAGGACAATTTAACAGAGAAATTTTTGTTGATGACGGTTAACAGAA [        :::	131 ABPLYBABNILELLEABNVALLEUTHRSEKILEVALTHRFROLLELYBABNGINLEUABP 150 484 AGCTATAATACAGCATTAGATGATTGAGAAAATTAAAAAGACTACAAGCTCCTGGATTA 543	544 CCACCATCACCATTACAACAACTGCCTTGACTCTTAAAATACGATTTGAGAATGTT 603 :::       :::       :::         :::	604 CACAATGATTITATTCGAGAATACCTGGTTTCCAACTTGAAACTTATAAA 654 :::	655 ACGCTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTACAACAA 714 	715 GGTGCTGAATTGGCTGATGGAATGCAATATACATCTTCACAAATTGAACCTAAT  217 AlaalaThrTyTrTyTyTAGATTATAAACTTTTAAAGAAAATATACTAAATAATAGT 831  775 GCTGGAACATCACATTATAAACTTTTAAAGAAAATATACTAAATAATAGT 831  324 ThrPheAsnSerSerAsnTyTrYrGlnGlyTyTceuLysArgLysIleGlnGluTyTrThr 253  832 AACTATTGTCAAATACTATAGAAAGAAATAAAACTTCGAAACCTAATATG 891  234 ThrPheAsnSerSerAsnTyTrYrGlnGlyTyTceuLysArgLysIleGlnGluTyTrThr 253  832 AACTATTGTCAAATACTATAGAAAGAAATAAAAAATATAGAAACTACTAATATGT  254 AspTyrCysIleGlnThrTyTrAAGATAATACAAATAATACTAATAAAAAATAAAAAATAAAAAA
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	1819 TCTACACAATCTTATTACATTAGACTTCGATACGACAAATGCTGGAAATACTTTTACATTCGATACGCTACAAATGGTGCTGGAAATACTTTTTACATTAGACTTCGATACGCTACAAATGGTGCTGGAAATACTTTTTTTT	1879 CCTANIANTCTTACANTACAGGANTANTAGGANTACCACCTCAGGACTCAACAAC  18.1	DD 621 Infrhesergifinfabilyfinfabnleddy81yflygaagpheGin1yfledGiuphe 640 Qy 1999 CCAAGTACAGTAACATTACCTTTAAATCGAACATTACATTTAATCTTAATCGTGCAGAT 2058  1::	Oy 2059 GTATCAAAITTGAATTTTAATCATTGATAAATTGAATTTATACCAATTACTTCCTCT 2115	Oy 2116 GTACGCCAAAATAGAGAAAAAATTAGAAACTATCCAAACAAA	Qy 2176 TTCACAAATCATACAAAATACTTTAAATATAGAAGCCACAAACTATGATATTGAT 2232 :::	RESULT 3 Bazegoral crystal protein - Bacillus thuringiensis subsp. israelensis (fragment) C,Species: Bacillus thuringiensis subsp. israelensis C,Accession: B29338 A;Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticida A;Rocession: B29338 A;Rocession: B29338 A;Rocession: B29338 A;Rosldues: 1-934 cTHO A;Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticida A;Rocession: B29338 A;Rocession: B293

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ορ	360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla373	ě
ò	1219 AGÀTCTACTTATGCTACGACAGGAACTGAAATTATATATGGAGAAGAACAGGT 1272	8 8
g G	374PheThrHisThrAsnAspAspArgAsnileileTrpGlyAlaValHisGlyAsnile 392	Š
රි රි	CCACCCACAACAAAAACCATTAATACCATTTGAATCCTATAAAGTT	2 음
8 8	1.esercinaspinrserly8valPheProPhelyYargAshuy8ProlieAsply8val	RES
s a	1318 TCMATITAMCTRATCHANGTAMCTICCCTTTTTCCTAMCTTTAMC 13// 	par N,A
ò	1378 ATTAATCAAATTGAACTTTATTTAAATAATTCACCTAGTAATAAATTAACATATTCAGCT 1437	ວິດ
q	423 IlelleTyrGluMetilePheBerAgnSerSerGluValPheArgTyrSerSer 441	2,5
È	1438 GGGGGAAITTAICTAAIGATAAAAAAAAACAACIGAITTITCAAITITCCIGTAAAAAAGAC 1497	A,T
qq	442 AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr 461	A A
ò	TGTAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTATAGTCATATTTTA	A A
셤	462 TrpLys	R;Y
Š	1558 TCCCAGTITICTITATITATICCTAIAAAAITGGATIAGCCCTAAAIAIAIAI 1617	A;T
<sub>면</sub>	472 SerTyrıleLysThrAspAsnTyrılePheSerValValArgGluArgArg 488	A; A
È	1618 ACAGGIGCATTAGGACGACACACAGTAGTAATAGAAATAATGCAATATCAGATAAA 1677	A, R
qq	489 ArgValAlaPheSerTrpThrHisThrSerValAspPheGlnAsnThrileAspLeuAsp 508	Aid
È	1678 ATAATTACAATGATCCAGCAATCAAAGGTAACAGTCTGATACAAACTCTAAGGTAATT 1737	A . R
qq	509 AsnileThrGlnileHisAlaLeuLysAlaLeuLysValSerSerAspSerLysIleVal 528	A; A
È	1738 GAAGGACCTGGTCATACAGGAGAACTTGGTTTATTTACAAAGTCAAGGCGTTTAGAG 1797	R, 1
q	529 LysdlyProdlyHisThrdlydlyAspLeuVallleLeuLysAspSerMetAsp 546	A; A
ò	1798 ATTACATGTAGAACTCCTAATTCTACACAATCTTATTACATTAGACTTCGATAGGCT 1854	AA
ብ	547 PheArgValArgPheLeuLyBAsnValSerArgGlnTyrGlnValArgIleArgTyrAla 566	A;F
È	ACAAATGGTGCTGGAAATACTCTTTCCTAATATACTCTTTACAATACCAGGGAAATAGGA	R; S
д	567 ThrAsnAlaProLysThrThrValPheLeuThrGlyIleAspThr 581	A; A
È	1915 ATACCACCTCAACGACTCAACACTTTTTCTGGTACAATTATAAATAATTTA 1968	A
q	582 ileserValGluLeuProserThrThrSerArgGlnAsnProAsnAlaThrAspLeu 600	A
ò 1	CAATAGGGAATTTTGGGTATTTCCAAGTACAGTA	A K
g	oul inriyralaasprneelylyrvalinrrnerroarginrvalrroashnysinrrneelu olu	A;1
È	2011ACATTACCTTTAAATCGAAACATACCATTTATATTTAATCGTGCAGATGTA 2061	A; A
<del>Q</del>	621 GlyGluAspThrLeuLeuMetThrLeuTyrGlyThrProAsnHis 635	A Y
È	2062 TCABATTCAATTITAATCATTGATAAAATTGAATTTATACCAATTACTTCCTCTGTACGC 2121	A;F
ą	636 SertyrAsnileTyrileAspLysileGluPheileProileThrGlnSerValLeu 654	ີ່ວ່ວ
È	2122 CAAAATAGAGAAAAACAAAAATTAGAAACTATCCAA	ີ່ວ່
<del>Q</del>	655 AspTyrThrdluLysdlnAsniledluLysThrdlnLysIleValAsnAspLeuPheVal 674	Ali
È	2158 2166	Sco
<del>Q</del>	675 ABRABRILYBValLeuThriyBileABpSerMetAlaValLyBLyBAlaArgLyBValVal 694	Be

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Alternate names: delta-endotoxin Bt8; insecticidal protein ISRH3; mosquitocidal 130K p. Alternate names: delta-endotoxin Bt8; insecticidal protein ISRH3; mosquitocidal 130K p. Species: Bacillus thuringiensis subsp. israelensis
.Species: Bacillus thuringiensis subsp. israelensis
.Species: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 05-Oct-2004
.Accession: 800398; A37587; JT0315; A28541; 139869; I40554
.Chungjatupornchai, W.; Hoefte, H.; Seurinck, J.; Angsuthanasombat, C.; Vaeck, M.
Ix. J. Blochem. 173, 9-16, 1988
.Title: Common features of Bacillus thuringiensis toxins specific for Diptera and Lepid Accession: 800398; MUID:88185334; PMID:283395
.Accession: BNA
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Molecule type: DNA

Molecule type: Molecule type
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is toxic to many lepidopteran larvae.
Superfamily: Parasporal crystal protein
Keywords: delta-endotoxin
2167 AATACATTTTTCACAAATCATACAAAAATACTTTAAATATAGAAGCCACAAACTATGAT 2226
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Matches:
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CCCACAACAAAAACTTTAATACCATTTGAATCCTATAAAGTTTCAATTGTAACTGATAGA 1335
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                                                                                                                                                                                                                                                                             777
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                                                                                                                   GGATTACCACCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAG 597
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                                                                                                                                                                                                                                                    201 LeuPheLeuProThrTyrAlaGinAlaAlaAsnThrHisLeuLeuLeuLeuLysAspAla
                                                                                                                                                                                                                                                                                                                                 GGAACATCAGATGAC-----TATTATAAACTTTTAAAAGAAAATATATATAT
                                                                                                                                                                                                                                                                                                                                               269 AspAlaTrpValLysPheAsnArgPheArgArgGluMetThrLeuThrValLeuAspLeu
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ThrileAlaAsnThrAspIleAlaAlaPheProAspGlyLyVsIleTyrPheGlyValThr
                            598 AATGTTCACAATGATTTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAAACG
                                                                                                                                                                                                                          CTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATACAACAAGGT
                                                                                                                                                                                                                                                                              GCTGAATTGGCTGATGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCT
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                                                                TTACAAAGCTATAATACAGCATTAGATGATTGAAGAAAATTAAAAAAGACTACAAGCTCCT
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810228
parasporal crystal protein cry3Bal - Bacillus thuringiensis (fragment)
NyAlternate names: coleopteran-active parasporal crystal protein; delta-endotoxin
C;Species: Bacillus thuringiensis
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C;Accession: $10228
R;Sick, A.; Gaertner, F.; Wong, A.
Nuclect Acids Res. 18, 1305, 1990
A;Title: Nucleotide sequence of a coleopteran-active toxin gene from a new isolate of Ba
A;Reference number: $10228, MUID:90206811; PMID:2320431
A;Reference number: $10228
A;Retus: translation not shown
A;Redues: cry1118
C;Genetics:
A;Gene: cry111B
C;Reywords: delta-endotoxin; toxin
                                         GAACAAGACAAAACAGTATGGACACAATTTATTAAAATGGGAGAAATTTTTGTTGATACA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTTCTAACAGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACCA 117
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ProThrasn------HisasnGlnTyrProLeualaaspasnProAsnSerThr
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|LeuGluGluLeuAsnTyrLysGluPheLeuArgMetThrAlaAspAsnSerThr-----
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Query Match:
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1435 GCT		AATCAAA :::    IValLys AGGAAAC         YGlyAsn TAGAACT	rggaart 1	H H-0 4.0	04 .; Johnson, T.; Becticidal cry :g142729; PIDN
ែលដឹងព័ថ៌យកិស័ប្រែបប្រឹក្សាប្រជា		ACTGTTAATAGAAATAATGCAATAATGAAAAATAATTACAATGAATG	CCTAATTCTACACAATCTTATTACATTAGACTTCGATACGCTACAAATGGTGCT  AlaAlaLeuLeuGlnArgTyrArgValArgIleArgfyrAlaSerThr  ACTCTTCCTAATATATCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAA  ACTCTTCTTCTGCAATACCAGGAGTAATAGGAATACCACTCAA ThrA8nLeuArgLeuPheVal	594 AsnAsnPheLeuValileTyrileAnLysThrMetAs 1987 TATTTCCAATTTCCAAGTACAGTACATTACCTTT 614 TyrGlnThrPheAspPheAlaThrSer	RESULT 6 139811  Datasporal crystal protein cry3Bbl - Bacillus thuringiensis  N.Alternate names: parasporal crystal protein cry1IB2 C/Species: Bacillus thuringiensis C/Species: Bacillus thuringiensis C/Accession: I3981  R/DDONOVAD, W.P.; Rupar, M.J.; Slaney, A.C.; Malvar, T.; Gawron-Burks, Appl. Environ. Microbiol. 58, 3921-3927, 1992 A/Title: Characterization of two genes encoding Bacillus thuringiensis A/Appl. Environ. Microbiol. 58, 3921-3927, 1992 A/Accession: I39811 A/Accession: I3981

Alignment Scores:

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.; Annys, K.; Jansens, S.; Soetaert, P.; Peferoen, M.
1. 58, 2536-2542, 1992
thuringiensis insecticidal crystal protein with a silent activit
344; MUID:92384571; PMID:1514800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROT:Q03749; UNIPARC:UPI000002C1B6; GB:M64478; NID:g142760; PIDN:
ted from NCBI backbone (NCBIN:112092, NCBIP:112093)
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                                                       STAACATTACCTTTAAATCGAAACATACCATTTATATTTAATCGTGCAGAT 2058
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AATATTGATCATTCT --- AGATACCCTTACACAAATAATCCAAATCAACCA 117
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|etAsnTyrGlnAspPheLeuSerIleThrGlu------Arg 46
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|SluAlaLeuAlaSerGlyAsnThr-----AlaIleAsnThrValValSer 64
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                                                                                                                               CAATTTTAATCATTGATAAATTGAATTTATACCAATT 2106
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1716
1480 TTTCCTGTAAAAAAAGGCTGTAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAAT 1539
                                                                                                     1597 TTAGCGCTAAATATATATATACAGGTGCATTAGGATGGACACACAGTAGTGTTAATAGA 1656
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                                                                                                                               473 AsnAlaThrIleProIlePheSer------TrpThrHisArgSerAlaGluTyr 488
                                                                                                                                                                       528
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                                                                  1657 AATAATGCAATATCAGATAAATAATTACAATGATCCCCAGCAATCAAAGGTAACAGTCTT
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Paragoral crystal protein cry8Cal - Bacillus thuringlensis
NyAlternate names: parasporal crystal protein cryIII
NyAlternate names: parasporal crystal protein cryIII
C;Species Bacillus thuringlensis
C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Oct-2004
C;Accession: 140589
R;Sato, R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; Asano
Curr. Microbiol. 28, 15-19, 1994
A;Title: Cloning, heterologous expression, and localization of a novel crystal protein g
A;Reference number: 140589; MUID:94100786; PMID:7764305

8 8 8

A; Accession: 140589

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1160 <RES>

A;Residues: 1-1160 <RES> A;Cross-references: UNIPROT:Q45706; UNIPARC:UP10000126CFE; EMBL:U04366; NID:g532523; PID: C;Superfamily: Parasporal crystal protein

C;Keyword	ls: delta-endotoxin	oxin		;			;
Alignment Pred. No.: Score:	Scores:	2.85e-36 672.00	Length: Matches:	1160 216			8 8 8
Best Loca Query Mat DB:	Best Local Similarity: Query Match: DB:	27.55# 17.06# 2	Mismatches: Indels: Gaps:	317 128 29			8 8 8
US-10-782	-570-1 (1-223	5) x I40589 (1-	-1160)				8 8
<u>\$</u> 8	1 GTGAATCAA ::::: 1 MetSerPro	AATAATAATAATGA          AenAenGlnAenGl	GTGAATCAAAATAATAATGAATATGAGATTATCGATTCAAAGAATTTATCTTATCCT :::::	CAAAGAATTTAT	CTTATCCT 60	.,	\$ 8 ¢
<u>&amp;</u> 8	61 TCTAACAGA    ::: 21 SerAspAsn	AATATTGATCATTC :::     Serile	TCTAACAGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACCATTA	ATAATCCAAATC   :::  snaspglnThra	AACCATTA 120     snThrLeu 37		<b>8</b> 8
ර යි	121 CAAAACACA        38 GlnAsnMet	AATTACAAAGAGTG         ::::: .AenTyrlyeAepTy	CAAAACACAAATTACAAAGAGTGGCTCAATATGTGTGAAGGGAATACACAATATGGT 	GGAATACAC     erThrAenAlaG	AATATGGT 177 :: !uLeuSer 57		<u>රි සි</u>
දු පු	178 GATAATTIC     58 ArgAsnPro	GAGACATTTGCTAG         X1yThrPhe11eSe	GATAATTTCGAGACATTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATT	CAGTTAGTGCAG	STACTATT 237     Yileasp 75		8 8
සි ර	238 GTATCCGGT::: 76 IleValSer	ACTCTGTTAGCCGG    :::::::    Thr1le1leSerGl	Gracoggracocogratadgocogorocacococogradaa	CTATATCCGGAC	CGATAGGA 297     IlePro 87		è 8
දු පු	298 ATAATAGGT :::::	GCTATAATAATATC ::: GluValPheSerIl	ATAATAGGGGCTATAATAATATCTTTTGGTACCCTAATCACTGTCTTTTGGCCCGGGGA ::::::	ACTGICITITICGC ::: 1)	CCCCGCA 357   ::: roSerAsn 107		රි සි
<b>è</b> 8	358 GAACAAGAC :::::: 108 AsnGluAsn	AAAACAGTATGGAC         valtrpg1	GAACAAGACAAAACAGTATGGACACAATTTATTAAAATGGGAGAAATTTTTGTTGATACA 	GAGAAATTTTTG     alGluGluLeuI	41	5	& A
<u>\$</u> 8	418 CCGTTAACA ::: 126 Ly@ileLeu	GRAAGCATAAAACA :::   ::::: :AspSerValArgSe	CCGTTAACAGAAAGCATAAAACAGCTAAAGTTACAAACTTTAGAAGGATTTAGACAAATA 	rtagaaggattta      eualaasnSera	GACAAATA 477    rgileala 145	2	& 6 &
දු දු	478 TTACAAAGC ::::::	TATAATACAGCATT      TyrGlnAenAlaLe	TTACAAAGCTATAATACAGCATTAGATGATTGGAGAAAATTAAAAAGACTACAAGGCTCCT :::::	TTAAAAAGACTAC	53	8	충 A -
රු සි	538 GGATTACCA 159Agn	CCATCATCAGCATT          ProHissetthr	GGATTACCACCATCAGCATTACAACAAGCTGCCTTGACTTTAAAATACGATTTGAG 	ACTCTTAAAATAC :::      :euValLysGluA	59	<i>C</i> 4	& <b>a</b>
රු සි	598 AATGTTCAC     175 AsnAlaGlu	AATGATTTTATTCG AlaileLeuArgTh	AATGTTCACAATGATTTTAATTCGAGAAATACCTGGTTTTCCAACTTGAAACTTATAAAACG 	AACTTGAAACTT	19	F 44	8 8
දු දු	658 CTATTACTA	CCTATTTATGCGCA                Prothrtyralagl	CTATTACTACTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATACAACAAGGT	TTAAATTTATTAC     	17	7 4	& A
දු දු	718 GCTGAATTG 215 GlnIleTyz	GCTGAATTGGCTGATGAATGGAATGC        GlnIleTyrGlylysGluTrpGly	GCTGBATTGGCTGATGBATGGAATGCAGATACATCCTTCACAAATTGAACCTAATGCT 	rcacaaattgaac 31n	77	5	දු පු
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රු සි	838 TGTGCAAAI     246 Cy8ValGln	racctatagagaagg      TrpTyrAgnalagl	TGTGCAAATACCTATAGAGAGGACTAAATAAACTTCGAAACGAACCTAATATGAGATGG 	aacgaacctaata 31ythrg1ya1al	TGAGATGG 897 :::    yeGlnTrp 265	5	දි දි
È		Faatgattatcgaag	AGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACTATCGCTCAA	STATTAGATACTA	TCGCTCAA 957		ò

1297 -----CCATTTGAATCCTATAAAGTTTCAATTGTAACTGATAGACAAGTAACTCCTACT 1350 1885 ATATCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAAC 1938 1132 AGATTATTTTCATTTTTAGATGAACTTATA------TTTTATACAAAAAATGAA 1179 1240 GGAACTGAAATTATATATATGGAGAAAGAACAGGTCCACCACAACAAAAACTTTAATA--- 1296 1432 TCAGCTGGGGGGAATTTATCTAATGATAAAAAAAAAAATTTTCAATTTCCTGTAAAA 1491 1612 TIATATACAGGTGCATTAGGATGGACACACAGTAGTGTTAATAGAAATAATGCAATATCA 1671 1732 GTAATT-----GAAGGACCTGGTCATACAGGAGGAAACTTGGTTTATTTACAA 1779 1072 TACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAAATTTAACACGTTCAGGGCTT 1131 1180 ACGTACGGGAATCGTTTAGTTGGTATTGCGAATCGTAATAGATCTTATGCTACGACA 1239 1351 TCCCCT-----TTTCCTAACATATAC 1371 1372 ITTACAATTAATCAAATTGAACTTTAATTAATAATTAATTCACCTAGTAATAAATTAACATAT 1431 1552 ATTITATCCCAGITTTCTTTATTTAATTTCCTATAAATTGGATTAGCGCTAAATAA 1611 1672 GATAAAATAATTACAATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAAACTCTAAG 1731 1780 AGTCAAGGG------CGTTTAGAGATTACATGTAGAACTCCTAATTCTACACAA 1827 958 TITICITITIAIGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGCATTAAA 1017 1018 ACT-----GAACTTACAAGAGAAATTTATACAACTGAAATAAATTTTGACCGTCTTACT 1071 1492 AAAGACTGTAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTATAGTCAT 1551 266 ValAspTyrAsnArgPheArgArgGluMetAsnValMetValLeuAspLeuValAlaLeu 285 286 pheProAsnTyrAsp---------AlaArgIleTyrProLeuGlu 297 298 ThrasnalaGluLeuThrargGluIlePheThraspProValGly------Ser 313 |||::: ||| ::: ||| 333 | 333 | 334 TyrValThrGlyGlnSerSerThrLeuIleSerTrpTyrAspMetIleProAlaAlaLeu ||| 354 Glulle-------Gridham 364 ||| 385 GlySerSerPheAsnLysTyrSerGlyValLeuAlaGlyAlaGluAspIleIleProVal 404 405 GlyGlnAsnAspIleTyrArgValValTrpThrTyrIleGlyArgTyrThrAsnSerLeu 424 510 AlaThrLysIleSerGlnIleProlleAsnLysAlaSerArg----ThrSerGlyGly 527 

	333 PheserdilleudilleadlabheileArgProbloHedeuPheAspArgLeuAenSer 352 1114 TTAACAGTTCAGGGCTAGATATTTTCATTTTTAGATGACTTATATT 1164 1115 TATACAGAAAAAGGAATGATATTTTCATTTTTAGATGACTTATATT 1164 1165 TATACAAAAAATGAAAGGGGAATCGTTTAGTT
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Db 587 ArgSerProGluMenProAlathrYpSerAlaSerIleAlaTyThrAmThrNetSer 606  Oy 1999 ACTTTCTCGGLAATATATATATATACAAACAACAAATATTCGATTTTT 1999  Db 607 ThrAmDhaSerLeuthrYpSerThrAcAAACACACAATTTAATTTAATCGTCAATT 2099  CON ThrAmDhaSerLeuthrYpSerThrAcAAACACATTTAATTTAATCGTCAATT 2016  622	

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                                                                              1321 ATTGTAACTGATAGACAAGTAACTCCTACTTCCCCTTTTCCTAACATATACTTTACAATT 1380
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393 IleThrThrArgAlaThrIleAsnProGlyValAspGlyThrAsnArgIle-----
                                                 --GluserThralaValAspPheArgSerAlaLeuIleGly
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                                                                                                                                                                                                                                                                        450 ArgAspLeuTyrAspThrAsnAspGluLeuProProAspGluSerThrGlySerSerThr
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691 AsplyrGlnValAsp 695

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A; Molecule type: DNA
A; Residues: 9-652 cHOB>
A; Cross-rences: 9-652 cHOB>
A; Cross-rences: Var. tenebrionis
A; Experimental source: var. tenebrionis
B; McPherson, S.A.; Perlak, F.J.; Fuchs, R.L.; Marrone, P.G.; Lavrik, P.B.; Fischhoff, D.
Bo/Technology 6, 61-66, 1988
A; Title: Characterization of the coleopteran-specific protein gene of Bacillus thuringie
A; Reference number: A29987
A; Accession: A29887
A; Residues: 9-652 cMCP>
A; Residues: 9-652 cMCP>
A; Cross-references: UNIPARC: UP1000002B8CD
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R;Sekar, V.; Thompson, D.V.; Maroney, M.J.; Bookland, R.G.; Adang, M.J.
Proc. Natl. Acad. Sci. US.A. 84, 7036-7040, 1987
A;Title: Molecular cloning and characterization of the insecticidal crystal protein gene
A;Reference number: A28407
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A; Mesidues: 9-652 <58K5.
A; Residues: 9-652 <58K5.
A; A; Cross-references: UNIPARC: UP1000002B8CD
A; Experimental source: var. Tenebrionis
A; Experimental source: var. Tenebrionis
A; Experimental source: var. Tenebrionis
A; Adams. L.F.; Anthewes: 8; O'Hara, P.; Petersen, A.; Guertler, H.
Mol. Microbiol. 14, 381-389, 1994
A; Title: Rlucidation of the mechanism of CryIIIA overproduction in a mutagenized strain
A; Reference number: $60781; MUID:95131759; PMID:7830581
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A;Accession: $60781
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DAA
A;Molecule type: DAA
A;Accessives: 9-652 ADA>
A;Cross-references: UNIPARC:UPI000002B8CD; EMBL:U10985; NID:G506182; PIDN:AAC43266.1; PI
A;Cross-references: UNIPARC:UPI000002B8CD; EMBL:U10985; Outer receptor binding domain of Bacillus thu
A;Reference number: 862317; MUID:96163559; PMID:8568902
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Wol. Gene. 214, 365-372, 1988
A;Title: Isolation and characterization of EG2158, a new strain of Bacillus thuringiensı
A;Reference number: 139812; MUID:89112139; PMID:3146015
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R;Hoefte, H.; Seurinck, J.; Van Houtven, A.; Vaeck, M.
Nucleic Acids Res. 15, 7183, 1987
A;Title: Nucleotide sequence of a gene encoding an insecticidal protein of Bacillus thur A;Reference number: A26853; MUID:88015559; PMID:3658680
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                                                             cryC;
parasporal crystal protein cry3Aal - Bacillus thuringiensis
N;Alternate names: coleopteran-specific insect control protein; crystal protein cryC;
C;Species: Bacillus thuringiensis
C;Date: 19-Nov-1988 #sequence revision 19-Nov-1988 #text_change 05-Oct-2004
C;Accession: A27323; A26853; A29987; A28407; S60781; I39812; I39813
R;Herrnstadt, C.; Gilroy, T.B.; Sobieski, D.A.; Bennett, B.D.; Gaertner, F.H.
A;Title: Nucleotide sequence and deduced amino acid sequence of a coleopteran-active A;Reference number: A27323; MUID:88112860; PMID:2828180
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A; Residues: 1-652 < HER>
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AGAAATAATGCAATATCAGATAAAATAATTACAATGATCCCAGCAATCAAAGGTAACAGT 1713
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---AlaGluPheTyrLy8ArgGlnLeuLy8LeuThrGlnGluTyr
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        CCTAATGCTGGAACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATAT
                                                             AGTAACTATTGTGCAAATACCTATAGAGAAGGACTAAAATAAACTTCGAAACGAACCTAAAT
                                                                                                               ATGAGATGGAGTATATTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACT
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: 9-58 < REZ>
A; Cross-references: UNIPARC:UP100000B007B; GB:L03393; NID:g304150; PIDN:AAA22350.1; |
A; Genetics:
A; Genetics:
C; Superfamily: Parasporal crystal protein
C; Keywords: delta-endotoxin
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-----GlyAlaLeuValSerPheTyrThrAsnPheLeuAsnThr1leTrpProSerGlu 111
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ProThrAsn------HisValGlnTyrProLeuAlaGluThrProAsnProThr 44
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301 ATAGGIGCTATAATAATATCTTTTGGTACCCTAATCACTGTCTTTTGGCCGGGGAGAA 360			127 ArgalaryrdindinserLeudinaBpirpLeudiu	601 GTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAAACGCTA 660	661 TTACTACTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTTATTACAACAGGTGCT 720         :::	721 GAATTGGCTGATGAATGGAGATATACATCCTTCACAAATTGAACCTAATGCTGGA 780    ::: 196 LeuPheGlySerGluPheGlyLeu	781 ACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATATAGT 831        :::        :::        :::	832 AACTAITGIGCAAATACCTAIAGAGAAGGACTAAATAAACTICGAAACGAACGTAATAIG 891 	892 AGATGGAGTATATTAATGATTATCGAAGATATAATGACTATTACTGTATTAGATACTATC 951	952 GCTCAATTTTTTTTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGC 1011	1012 ATTAAAACTGAACTTACAAGAGAAATTTATACAACTGAAATAAAT 1056 	ATAAT laala		SerSerArgTrpSerAenThrArgH1eMetThrTyrTrpArgd1yH1eThrIleGlnSer	CGTTTACTTGGTATTGCGAATCGTAATAGATCTATGCTAGGTACGACAGGAATT 125. 	1252 ATATATGGGGAAGAACGGTCCACCCACAACAAAACTTTAATACCA 1299 
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Db 548 CysThrGluasnGlySeralaalaThrIleTyrValThrProAspValSerTyrSerGln 567  Cy 1828 TCTTATTACATTAGACTTCGATACGCTACAAATGGTGCTGGAAAATACTCTTCCTAATATA 1887  Db 568 LysTyrSacalaarGleHistyrValaSerThrserGlile 581	1888 TCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAACAACAACTTTTTCT :::    :::         582 ThrPheThrLeuSerLeuAspGlyAlaProPheAsnGlnTyrTyrPhe	1948 GGIACAAATTATAATAATTTACAATACGGAGATTTTGGGIATTTCCAATTT	OY 1999 CCANGIACAGIACAGIACACITIAANICCANACAAACAACCAITIAIAITIAAICGIGCAGAI 2058 1:::  Db 618 SerThrFroPheGluLeuSerGlyAsnAsnLeuGlnileGlyValThrGlyLeuSer 636  Oy 2059 GTAICAAAITCAATITTAATCAITGAIAAAITTAAACCAIT 2106	Db 637 AlaGlyAspLysValTyrlleAspLysIleGluPhelleProVal 651 RESULT 11		C.Accession: Sop. 1-3-0 Heduence_revision 0/-sep-1330 #text_cnange 03-0ct-2004 C.Accession: S00873 R.Brizzard, B.L.; Whiteley, H.R. Nucleic Acids Res. 16, 2723-2724, 1988	A;Title: Nuclectide sequence of an additional crystal protein gene cloned from Bacillus A;Reference number: \$00873; MUID:88203216; PMID:3362680 A;Accession: \$00873 A;Accession: \$00873 A;Molecule type: DNA	A; Keblades: 1-1228 ARL; A; Keblades: 1-1228 ARL; C;Genetics: A;Gene: cryA4	Ajstart codon: TTG CjSuperfamily: Párasporal crystal protein CjReywords: delta-endotoxin	Alignment Scores: Pred. No.: 4.87e-32 Length: 1228 Score: 607.00 Matches: 209 Percent Similarity: 46.32% Mignative: 114 Best Incal Similarity: 26.04% Mignative: 244	15.41% 2 235) x 800873 (1-12	1 GTGATCAAAATAATAATAA 1::	61 TCTAACAGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACCATTA	Qy 121 CAAAACACAAATTACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGTGAT 180 121 CAAAACACAAATTACAAAGGAGTGGTCAATATGGTGAT 180 Db 27AspalaArgIleGluAspSerLeuCysIleAlaGluGlyAsn 40	Qy 181 AATTTCGAGACATTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATTGTA 240	Qy 241 TCCGGTACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGAATA 300 :::    :::    :::    Db 58 AlaGlyArg1leLeuGlyValLeuGlyValProPhe 69

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1420 AAATTAACATATTCAGCTGGGGGAATTTATCTAATGATAAAAAACAACTGATTTTCAA 1479
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TTTGAATCCTATAAAGTTTCAATTGTAACTGATAGACAAGTAACTCCTACTTCCCCTTTT 1359
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------ProPheThrGlnIleGlnAgpIleIleArgThrSerIle
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|ThrGluSerTyrAlaGlyValLeuLeuTrpGlyIleTyrLeuGluProIleHisGlyVal
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| LeuglnSer-----ArgValAsnValProValTyrSer------
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127 AspLeuLysGlyLeuGlyAspAlaLeuAlaValTyrHisAspSerLeuGluSerTrpVal 146
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LeuProSerPheAlaValSerGlyGluGluValProLeuLeuProlleTyrAlaGlnAla 192
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insecticidal protein cryV - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 05-Oct-2004
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insecticidal protein cryV1 - Bacillus thuringlensis

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() Species Bacillus thuringlensis

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Appl. Environ. Microbiol. 61, 2402-2407, 1995

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Appl. Environ. Microbiol. 61, 2402-2407, 1995
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A;Gene: cryV1
C;Superfamily: Parasporal crystal protein
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Cross-references: UNIPROT:P19415; UNIPARC:UPI000002C0A3; EMBL:X54160; NID:g Superfamily: Parasporal crystal protein Keywords: delta-endotoxin  diament Scores:	100	Qy 211 ATTGCTGCAGTACTACTACTAGTATCCGGTACTCTGTTAGCCGGTATA 264    ::	<pre>3luLellFTpGlyPhelleGlyPro 3GaGaAATTTTTGTTGATACACGTTAACAGAA 1leGluGlnLeulleSerGlnArglleGluGlu 1raGAAGGATTTAGAAATATACAAAGCTAT 1raGAAGGATTTAGAAATATACAAAGCTAT 1  </pre>	Qy         505 GATTGGAGAAATTAAAAGACTACAAGCTCCTGGATTACCACCATCATCATCAA         564           Db         115 AspTrpGluLys	Qy         685 GCTAATTTTCAITTTACAACAAGGGGGCTGAATTGGCTGATGGAATGCAATGGAATGCAATGGAATGCAATGGAATGCAATGAATG
441 GlyfyrAlaGlyfleGlyfhrGlnLeuGlnAspSerGluAsmGluLeuProProGluAla 460 1495 GACTGTAAACCAATTATTAATTGTTTACCAAGCTATAATAGTCATAT 155 ::: 461 ThrGlyGln	dy 1675 AAAATAATTACAGGAATCAAAGGTAACAACTCTTGATACAAGGTT 1734  Db 505 AenSerlleThrdlnIleProLeuvalLyBalaPheAenLeuSerSerGlyAlaAlaVal 524  Qy 1735 ATTGAAGGACCTGGTCATACAGGAGAAACTTATTACAAAGTCAAGGG 1788  Db 525 ValargGlyPrcGlyPheThrGlyGlyAspileLeuArgArgArrAstrActhrAsnThrPhe 544	QY         1789CGTTTAGAGATTACATGTAGAACTCCTAATTCTACACATTCTTATTACATT         1839           Db         545 GlyaspileArgValasnileAsnProProPheAlaGinArgTyTATgVal         561           QY         1840 AGACTTCGATACGCTACA	Db 582 IleAsnGlnGlyAsnPheSerAlaThrMet	Qy       2050 CGTGCAGATGTATCAAATTTTAATC	Qy 2194 AATACTTTAAATATAGAAGCCACAAACTATGATATTGAT 2232

රු දු	985 AAAGATTCAATAGGAAGAATAGGTGGCATTAAAACTGAACTTACAAGAGAAATTTATACA 1044 255 ProlleGlnThralaThrGlnLeuThrargGluValTyr 267	
È	1045 ACTGAAATAAATTTTGACCGTCTTACCTTGAAATTCAACCCAATCTCGCT 1098	
eg eg	268 LeudspleuProPhelleAsnGludsnfeuSerProAlaAlaSerTyrProThrPheSer 287	
<i>≿</i> *8	ATAATOGAATATATAACACGTTCAGGCTTAGATTATTTTCATTTTAGATGACTT	
g	AlaAlaGluserAlallelleArgserProHisbeuvalAspPhebeuAsnserPhe	
δí	ATATTTTATACAAAAAATGAAACGTACGGAATCGTTTAGTTGGTATTGCGAATCGTAAT	
g	307 ThrileTyrThrAspSer 312	
පි සි	1219 AGATCTACTTATGCTACGACAGGAACTGAAATTATATATGGAGAAGAACAGGTCCACCC 1278	
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දි සි	12/9 ACAACAAAAACTITAATACCATITGAATCCTATAAAGTITGAACTGAATAGACAA 1338 	
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ò	1396 TATTTAAATAATTCACCTAGTAATAAATTAACATATTCAGCTGGGGGGAATTTATCTAAT 1455	
q	371 LeuabpanSeranbrovalalaGlyIle380	
È	1456 GATAAAAAAACAACTGTTTTCCATTTTCCTGTAAAAAAAA	
qq	381GluGlyValGluPheGlnAsnThrIleSerArgSerIleTyrArgLysSerGly 398	
õ	1504 CCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGT	
Ωp	399 ProlleAspSerPheSerGluLeuProProGlnAspAlaSerValSerProAlaIleGly 418	
È	1543 TAIAGICATATITIAICCCAGITITICITIAITTAATTATITCCTATAAAAITGGAITAGGG 1602	
qq	419 TyrSerHisArgLeuCysHisAlaThrPheLeuGluArgIleSerGlyProArgIleAla 438	
ò	1603 CTAAATATTATATACAGGTGCATTAGGATGGACACACAGTAGTGTTAATAGAAATAAT 1662	
qq	439 GlyThrValPheSerTrpThrHisArgSerAlaSerProThrAsn 453	
È	1663 GCAATATCAGATAAAATTACAATGATCCCAGCAATCAAAGGTAACAGTTGTTGATACA 1722	
Db	454 GluValSerProSerArgileThrGlnileProTrpValLysAlaHisThrLeuAlaSer 473	
È	1723 AACTCTAAGGTAAITGAAGGACCTGGTCATACAGGAGGAAACTTGGTTTATTTA	
q	474 GlyalaSerVallleLysGlyProGlyPheThrGlyGlyasp1leLeuThrArgAsnSer 493	
à	1783 CAAGGGCGTTTAGAGATTACATGTAGAACTCCTAATTCTACACAA 1827	
qq	494 MetGlyGluLeuGlyThrLeuArgValThrPheThrGlyArgLeuProGln 510	
ò	1828 TCTTATTACATTAGACTTCGATACGCTACAAATGGTGCTGGA 1869	
qq	511 SerTyrTyrTleArgPheArgTyrAlaSerValAlaAshArgSerGlyThrPheArgTyr 530	
È	1870 AATACTCTTCCTAATATATCTTACAATACCAGAGTAATAGGAATACCACCTCAACGA 1929	
g g	531 SerGlnProProSerTyrGlylleSerPheProLysThrMetAspAlaGlyGluProLeu 550	
è	1930 CTCAACAACTTTTTCTGGTACAAATTATAATTTTACAATACGGAGATTTTGGGTAT 1989	
g	551 ThrSerArgSerPheAlaHisThrTheuPheThr552	

ò	1990	1990 ITCCAAITICCAAGIACAGIAACAITAACTITAAAICGAAACAIACCAITIAIAITAAI 2049	2049
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È	2050	2050 CGTGCAGATGTATCAAATTCTAAATCATTGATAAAATTGAA 2094	2094
Op Q	268	568 ArgAlaGlnGluGluPheAspLeuTyrIleGlnSerGlyValTyrIleAspArglleGlu 587	287
ò	2095	TITATACCAATTACTTCCTCTGTACGCCAAAATAGAGAAAAACAAAAATTAGAAACTATC	2154
ନ୍ଧ	588	588 PhelleprovalThralaThrPheGluAlaGluTyrAspLeuGluArgAla 604	604
ò	2155	2155 CAAACAAAATAATACATTTTCACAAATCATACAAAAAAAA	2214
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Ward B.S., Ellar D.J.;
"Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene
encoding a 130 kDa delta-endocxin.";
Nucleic Acids Res. 15:7195-7195(1987).
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-1- PUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sen K., Honda G., Koyama N., Nishida M., Neki A., Sakai H., Himeno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Komano T.;
Tcloring and nucleotide sequences of the two 130 kDa insecticidal
protein genes of Bacillus thuringiensis var. israelensis.";
Agric. Biol. Chem. 52:873-878(1988).
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01-AUG-1990 (Rel. 15, Last sequence update)
01-AUG-1990 (Rel. 15, Last sequence update)
13.SEP-2005 (Rel. 48, Last annotation update)
Pesticidial crystal protein cry4Aa (Insecticidal delta-endotoxin CryIVA(a)) (Crystaline entomocidal protoxin) (135 kDa crystal protein).
Name-cry4Aa; Synonyms-cryIVA(a), isrH4;
Bacillus thuringlensis subsp. israelensis.
Plasmid 72 KD.
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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-G=/Ganz_1/USFTO_gpool_p/US10782570/runat_12012006_060221_7515/app_query.fasta_1.2375
-DSCALIGNE-100 -TRR_SCORE=pct -TRR_NEN=100 -TRR_NIN=0 -ALIGN=15 -MODE=LOCAL
-ODCALIGN=200 -TRR_SCORE=pct -TRR_NEN=100 -TRR_NIN=0 -ALIGN=15 -MODE=LOCAL
-OUTRWT=pcc -NORM=ext -HRAPSIZE=500 -MINITN=0 -MAXIXN=200000000
-USER=US10782570 @CGN 11 1418 @runat_12012006_060221_7515 -NCFU=6 -ICFU=3
-NO_WMAP -LARGEQUERY -NGG_SCORES=0 -MINITN =0 -MAXIXN=200000000
-LOCATE - NORM=EXT - NGG_SCORES=0 -NORM=100 -LONGING
-DST TIMEOUT=120 -WARN TIMEOUT=30 -THRRADE1 -XGAPO=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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(c) 1993 - 2006 Compugen Ltd.
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375 ThrProAgnAgnPhePhe---ThrSerHisTyrAgnMetPheHisTyrThrLeuAspAgn 393
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              SerThrTyrileSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnValileSerThr 150
                                                                                                                                                                                     265 ValThrThrTyrLysLysGlyLeuAsnLeulleLysThrThrProAspSerAsnLeuAsp
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394 IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu
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                                                              TATAATACAGCATTAGATGATTGGAGAAAATTAAAAAGACTACAAGCTCCTGGATTACCA
                                                                                                          TyrHisAsnHisLeuLysThrTrpGlu------AsnAsnProAsnProGln
                                                                                                                                                         CCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAGAATGTTCAC
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AspLeuValAlaLeuPheProAsnTyrAspValGlyLysTyrProIle-----
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                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAAATTACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGTGATAATTTC 186
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                                       ğ
                                                                                                                            MISCELLANBOUS: Diverse amino acid mutations in sequence block 667-67 have no direct effect on the insecticidal activity but alter the structural stability of the toxin protein molecule. SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACCATTACAAAAC
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|GluThrPhelleAmpSer-----GlyGluLeuSerAlaTyrThrIleValValGly
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                                                                            MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part the spore coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> V (in Ref. 2).
-> I (in Ref. 2).
-> G (in Ref. 2).
-> W (in Ref. 2).
6FB5B6979DACAD3B CRC64;
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PRS; A26858.

PIR; 13870; 13870.

InterPro; IPR001178; Endotoxin.

InterPro; IPR00538; endotoxin.

Pfam; PR03944; Endotoxin.C; I.

Pfam; PR0355; Endotoxin.M; I.

Pfam; PR01955; Endotoxin.M; I.

Pfam; PR01979; Endotoxin.M; Pfam; Pfa
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MEDLINE=22235415; PubMed=12324359;
DOI=10.1128/AEM.68.10.5082-5095.2002;
DOI=10.1128/AEM.68.10.5082-5095.2002;
Berry C., O'Niel S., Ben-Dov B., Jones A.P., Murphy L., Quail M.A., Harris D., Zaritsky A., Parkhill J.;
"Complete sequence and organisation of pBtoxis, the toxin-coding plasmid of Bacillus thuringiensis subsp. israelensis.";
Appl. Environ. Microbiol. 6:5082-5095(2002).
EMBL, AL731825; CAD301481; -; GEDOMIC DNA.
SERGUENCE 1180 AA; 134538 MW, 6FB5E6979DACAD3B CRC64;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Pesticidial crystal protein cry4AA.
Name=cry4AA; Synonyms-cry1VA(A), isrH4, pBt110;
Bacillus thuringiensis (subsp. israelensis).
Bacteria; Pirmicutes; Bacillales; Bacillaceae; Bacillus;
CMB_TaxID=1430;
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01-MAR-2001 (TrEMBLrel. 16, Last seq
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ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn
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                                                                                                           GluSerProTyrLysTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg
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LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr
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GlyAspLeuIle-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn
                               CGTCTTACTTTACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAATTAACACGT
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-------AlaPheAlaSerPheValAsnPro-------GlyValValLeuIle 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=cry,

Name=cry,

Bacillus thuringlensis (subsp. finitimus).

Competia; Firmicutes; Bacillales; Bacillus;

Bacillus cereus group.

NCBI_TaxID=29337;

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(1)

RA

NOCE G.D., Debro L.H.;

RA

NOOR G.D., Debro L.H.;

RA

NOOR G.D., Debro L.H.;

REL;

RASP; QG0117; 1J16.

COMPACTOR FINYCOLORS CALVED GROUP.

BREL;

REL;

RESP; QG0117; 1J16.

COMPACTOR FINYCOLORS CALVED.

ROG; GC010016787; Finydrolase activity; IEA.

DR GO; GC0100103; Freeceptor binding; IEA.

CO; GC0100103; Freeceptor binding; IEA.

CO; GC0100103; Freeceptor binding; IEA.

CO; GC0100103; Freeceptor binding; IEA.

DR GO; CO0004055; Preceptor binding; IEA.

DR HIGEPRO; IPRO0653; endotoxin. C.

InterPro; IPRO0553; endotoxin. C.

DR Ffam; PRO0555; Endotoxin. N; 1.

DR Ffam; PRO0555; Endotoxin. N; 1.

DR Ffam; PRO0555; Endotoxin. N; 1.

PFam; PRO0555; Endotoxin. N; 1.

SQUENCE 1128 AA; 127450 MW; 61BODC9454BDF0E8 CRC64;
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Last annotation update)
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Matches:
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Oy 1447 TTATCTAATGATAAAA :::::	1612 461 1672 479 1732 198	Oy 1792 TTAGAGATTACATGTAGAACTCCTA  Db 516 CysSerIleLysCysLysAla		RESULT 4  C28A BACTF  ID 728A4 BACTF  STANDARD; FRT;  AC 03X682;  DT 16-OCT-2001 (Rel. 40, Last sequency of 13-SEP-2005 (Rel. 40, Last annotaty of 13-SEP-2005 (Rel. 40, Last annotation of 13
AAACAGCTAAAGTTACAAACTTTAGAAGATTTAGACAAATATTACAAAGCTATAATACAAACAGCTATAATACAAAGCTATAAAACAATTTAGAACAATTTAGAAAATTACAAAGCTATAAAAAAAA	132ABRThrAlaArgLeuValSerdInArgPheGluAsnAlaHisPheAsnPhe 148 616 ATTCGAGAATACCTGGTTTCCAACTTGAAACTTATAAAACGCTATTACTACTATTAT 675 618 :::	AATACCT               LysThrI   TTTAATG   TYTASSIT                   PheTyrA   CTTACAA	ATTATACAACT  ***I	
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AITITATACCAATTACTTCCTCTGTACGCCAAAATAGA 2130
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AAAACAACTGATTTTCAATTTCCTGTAAAAAAGAC 1497
                                                                             TGTTTACCAAGCTATAATAGT-----TATAGTCAT 1551
                                                                                                                                                          AATTATTCCTATAAAATTGGATTAGCGCTAAATATA 1611
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                                                                                                       AspTyrGlyGlySerAsnSerGlnLysPheLysHis 440
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|PheGlnTyrHisThrLeuLeuValAspileGluLeu 588
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|ProThrPheSerArgLysGlyAsnAsnAsnPheThr 568
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|PhelygProlleAspGluAsnTyr-----Thr 625
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GluThrThrAsnTyr------426
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stion updates
Aba (insecticidal delta-endotoxin
ocidal protoxin) (126 kDa crystal
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|ThraspTyrHisIleAsp 658
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nitimus.
; Bacillaceae; Bacillus;
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|AlaPheAsnAspTrpLysArg-----AsnProSerAla 131
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|SerSerAspThrValAlaValValSerAlaGlyIleValValValGlyThrIleLeuThr
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LysGlulleAlaLeuAlaHisLeuAsnGlyPheLysAspValLeuThrTyrTyrGluArg
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       MEDLINE-99330166; PubMed=10403372; DOI=10.1016/S0014-5793(99)00650-X; Mojciechowska J.A., Lewitin B., Revina L.P., Zalunin I.A., Wojciechowska J.A., Lewitin B., Revina L.P., Zalunin I.A., Chestukhina G.G., The novel delta-endotoxin gene families cry26 and cry28 from Bacilluc thuringieneis sep. finitimus., The novel delta-endotoxin gene families cry26 and cry28 from Bacilluc thuringieneis sep. finitimus., FEBS Lett. 453:46-48(1999).

-I- FUNCITON: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.

-I- BUNCITON: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.

-I- BUNCITOM: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.
                                                                                                                                            the spore coat. MISCELLANBOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                      10C80705508F5CDA CRC64;
                                                                                                                                                                               SIMILARITY: Belongs to the delta endotoxin family.
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240
106
242
114
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Matches:
Conservative:
Mismatches:
Indels:
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HSSP; Q06117; 1J16.
INTERPRO; PRO01179; Endotoxin.C.
InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin.C.
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SEQUENCE [GENOMIC DNA]
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Pfam; PF00555; Endotoxin M; 1.
Pfam; PF03945; Endotoxin N; 1.
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901.00
49.29%
34.19%
22.87%
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Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                     terminus.
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266 ArgArgPhePro------ArgGlyValGluLeuGluLeuThrArgGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      336 Asn------ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1534 TATAATAGT-----TATAGTCATATTTTATCCCAGTTTTCTTTATTTAATTATTCCTAT
                                                                                             TGGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCTGGAACATCAGATGACTAT
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TrpAsnAlaAspGlnProHisSerProMetLeuLysSerSerGlyThr------Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGAGATACAAAGATTCAATAGGAAGAATAGGTGGCATTAAAACTGAACTTACAAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ArgGluSerLysTyrThrGlyAsnGlnPhePheThrMetLysAsnIleTyrGly
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                                                                   GCGCAAGCTGCTAATTTTCATTTAAATTTACAACAAGGTGCTGAATTGGCTGATGAA
                                                                                                                                                                                                                                                                                                                                     GAAGGACTAAATAAACTTCGAAACGAACCTAATATGAGATGGAGTATATTTAATGATTAT
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us-10-782-570-1.rup

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SIMILARITY: Belongs to the delta endotoxin family
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Percent Similarity:
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SEQUENCE 6.
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                                                                  AACAGTCTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAGGAAACTTG 1767
                                                                                                                                                                                                                                                                                                                           1828 TCTTATTACATTAGACTTCGATACGCTACAAATGGTGCTGGAAATACTCTTCCTAATATA 1887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1948 GGTACAAATTATAATAAT------TTACAATACGGAGATTTTGGGTATTTTC 1992
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MEDLINE-86223796; PubMed=3011746;
MEDLINE-86223796; PubMed=3011746;
MEDLINE-86223796; PubMed=3011746;
Malfield A.M., Pollock T.J.;
"Structural similarity between the lepidoptera- and diptera-specific insecticidal endotoxin genes of Bacilius thuringiensis subsp. 'kurstaki' and 'israelensis'.';
J. Bacteriol. 166:801-811(1986)
-:- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of mosquitos. Active on Aedes aegypti.
-:- DEVELOPMENTAL STAGE: The crystal protein is produced during sportlation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::: |||||| ::: ||||| ThrLeuLeuValAspIleGluLeuProGluSerGluGluIleHisleHisLeuLysArg
      ValAsnSerGlnAsnLeuIleSerGluSerValSerThrGlnIleProLeuValLysAla
                                                                                                             ::: ||||||:::||| | TyrGluVal---ThrAsnAsnSerValIleArgGlyProGlyPheThrGlyGlyAspLeu
                                                                                                                                                                                                GTTTATTTACAAAGTCAAGGCCGTTTAGAGATTACATGTAGAACTCCTAATTCTACACAA
                                                                                                                                                                                                                                  LystyrAlaileSerLeuPheTyrAlaAlaAsnAsnAlaIleAlaValSerIleAspVal
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01-MAR-1989 (Rel. 10, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation)
14-SEP-2005 (Rel. 48, Last annotation)
15-SEP-2005 (Rel. 48, Last annotation)
17-SEP-2005 (Rel. 48, Last annotation)
17-SEP-2005 (Rel. 48, Last annotation)
18-SEP-2005 (Rel. 48, Last annotation)

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MISCELLANEOUS: Toxic segment of the protein is located in the N-
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGAATAATAGGTGCTATA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAGAATGTT 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuGly-----ValLeuAlaAlaPheAlaAlaPro----ValLeuAlaAlaGly 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||||||::||||||||||::|||||||
TyrLysAspTrpLeuAsnValCysGInAspAsnGInGInTyrGlyAsnAsnAlaGlyAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATTGTATCCGGTACTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ThrHisAlaAsnAlaLysAlaValHisAspLeuPheThrThrLeuGluProIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                            675
251
1114
268
128
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                       EMBL; M12662; AAA22614.1; -; Genomic_DNA.
PIR; B29838; B29838.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
                                                                                                                                                                                                                                                                                                                                                                      675 AA; 77761 MW;
                                                                                                                                                                                                                                                                        Pfam; PF03944; Endotoxin C; 1.
Pfam; PF00555; Endotoxin M; 1.
Pfam; PF03945; Endotoxin N; 1.
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897.00
47.96%
32.98%
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Query Match:
DB:
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1915 ATACCACCTCAACGACTCAACACTTTTTTTTGGGTACAAATTATAAT-----AATTTA 1968
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                                                                                                                                                                                                                                                                                                                                      2011 -----ACATTACCTTTAAATCGAAACATACCATTTATATTTAATCGTGCAGATGTA 2061
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MEDLINE=222345415; PubMed=12324359;

MEDLINE=22235415; PubMed=12324359;

MEDLINE=22235415; PubMed=12324359;

DOI=10.1128/AEM.68.10.5082-5095.2002;

Berry C., O'Niel S., Ben-Dov E., Jones A.F., Murphy L., Quail M.A.,

Harris D., Zaritsky A., Parkhill J.;

"Complete sequence and organisation of pBtoxis, the toxin-coding
plasmid of Bacillus thuringiensis subsp. israelensis.";

"Complete sequence and organisation of pBtoxis, the toxin-coding
plasmid of Bacillus thuringiensis subsp. israelensis.";

"Appl Environ. Microbiol. 68:5082-5095(2002).

EMBL, AL131825; CAD300981.; -; Genomic_DNA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0006952; P:edeceptor binding; IEA.

GO; GO:0004945; P:pethogenesis, IEA.

GO; GO:0004945; P:pethogenesis, IEA.

InterPro: IPR005639; endotoxin...

R InterPro: IPR005639; endotoxin...

R Pfam; PP00545; Endotoxin...

R Pfam; PP00545; Endotoxin...

R Pfam; PP00555; Endotoxin...

R Pfam; PP00555; Endotoxin...

R Pfam; PP00555; Endotoxin...
 529 LysGlyProGlyHisThrGlyGlyAspLeuVallleLeuLysAspSer-----MetAsp
                                                                                                                    GAAGGACCTGGTCATACAGGAAGAACTTGGTTTATTTTACAAAGTCAAGGCGTTTAGAG
                                                                                                                                                                               ||||||||
567 ThrAsnAla--------ProLysThrThrValPheLeuThrGlylleAspThr
                                                                                                     1798 ATTACATGTAGA---ACTCCTAATTCTACACAATCTTATTACATTAGACTTCGATACGCT
                                                                                                                                                                                                                                                                                                        601 ThrTyrAlaAspPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu
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Bacillus thuringlenais (subsp. israelensis).
Bacteria; Firmicutes; Bacillales; Bacillus;
Bacillus cereus group.
                                                                                                                                                                                                                                                                              1969 CAATACGGAGATTTTGGGTATTTCCAATTTCCAAGTACAGTA-
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Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
Pesticidial crystal protein cryloAA.
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QBKNV2;
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----ThrileThrGluLeuGluAsnGlyLeuThrArgAsnPro--- 339
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360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla-----373
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                                                                                                                                 ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLysArgLys1leGlnGluTyrThr 253
                                                                                                                                                                                        274 ThrTrpAsnMetTyrAsnThrTyrArgLeuGluMetThrLeuThrValLeuAspLeuile 293
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               GCTGGAACATCAGATGACTATTATAAA---CTTTTAAAAGAAAATATACCTAAATATAGT
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	lignment Scores: 2.4e-52 Length:	Matches: Conservative:	DEBL LOCAL SIMILATICY: 32.98 MISMACCHEB: 200 Query Match: 22.778 Indels: 128 DB: 2 Gaps: 32	US-10-782-570-1 (1-2235) x Q8KNV2_BACTI (1-675)	OY 13 AATAATAATGAATTATCGATTCAAAGAATTTATCTTATC	6 AanLysAanGluTyrGlullePheAanAlaProSerAanGlyPheSerLysSerAanAan	Qy 73 ATTGATCATTCTAGATACCCCTTACACAATAATCCAAATCAACCATTACAAAACACAAT 132   :::	133 TACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGTGATAATTTCGAGACA	Db 44 TyrLysAspTrpLeuAsnValCysGlnAspAsnGlnGlnTyrGlyAsnAsnAlaGlyAsn 63	193 TTTGCTAGTGCTGATACTGCTGCAGTTAGTGCAGGTACTATTGTATCGGGTACTTGTATCTGGTACTTGTATGTA	64 PheAlaSerSerGluInFileValGlyValSerAlaGlyIleLleValValGlyInFmeC	UY ZSS TIAGCCGGTATAGGTGGGCTCACTTTTATCCGGACCGATAGGAATAGAGGCTCTATA SIZ Dh R4 I-angly	414 PARAMENTAL PROPERTY OF THE	96 Ilelleserphedy/ThriedleserpleJhenGinGlyserksprokladsn	373 GTATGGACACAATTTATTAAAATGGGAGAAATTTTTGTTGATACACGGTAACAGAA	Db 115 ValTrpGlnAspLeuLeuAsnIleGlyGlyArgProlleGluGlule 130	QY 430AGCATAAAACAGCTAAAAGTTACAAACTTTAGAAGATTTAGACAAATATTACAA 483	lelleAsn	OY 484 AGCTATAATACAGCATTAGATGGATGGAGAAAATAAAAAGACTACAAGCTCCTGGATTA 543	Db 151 LygiyrGlnGluPhePheAspLysTrpGluProAlaArg	544 CCACCATCACCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAGAATGTT :::	164ThrHishlahahalaLysAlavalHishspbeuPhernrThrLeuGlubrolle	OY 604 CACAATGATITTATICGAGAAATACCIGGITTCCAACTITGAAACTIATAAA 654 Dh 182 IlebaniadaanMatanMataniadaanBanBanBanBanAlaSartvaaraIlebaniadaanBanBanBanBanBanBanBanBanBanBanBanBanB	655 ACGCTATTACTACCCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTACAACAA 71	70	AATGCAG	Db 217 AlaAlaThrTyrTyrAsnIleTrpLeuGlnAsnGlnGlyIleAsnProSer 233	775 GCTGGAACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATATAGT	234 ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLysArgLysIleGlnGluTyrThr	OY 832 AACTATTGTGCAAATACCTATAGAGAGGACTAAATAAACTTGGAAACGAACG	892 AGATGGAGTATATTAATGATTATCGAAGATATATGACTATTACTGTATTAGATATCTATC

CCACCTCAACGACTCAACACTTTTCTGGTACAAATTATAAT -----AATTTA 1968 ATCAAATTGAACTTTATTTAAATAATTCACCTAGTAATAAATTAACATATTCAGCT 1437 AGTITITCTITIATITIAATITATTCCTATAAATITGGATTAGCGCTAAATATATATAT 1617 SGTGCATTAGGATGGACACACACAGTAGTGTTAATAGAAATAATGCAATATCAGATAAA 1677 TTACAATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAAACTCTAAGGTAATT 1737 CATGTAGA---ACTCCTAATTCTACACAATCTTATTACATTAGACTTCGATACGCT 1854 ATGGTGCTGGAAATACTCTTCCTAATATATCTCTTACAATACCAGGAGTAATAGGA 1914 AATTITITITITATGATATAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGC 1011 AAACTGAACTTACAAGAAATTTATACAACTGAAATAAATTTTGACCGTCTTACT 1071 TTGAAATTCAACCCAATCTCGCTATAATGGAATATAATTTAACACGTTCAGGGCTT 1131 TATTTTCATTTTTAGATGAACTTATATTTTTATACAAAAAAT------1176 CGTAC-------GGGAATCGTTTAGTTGGGAATCGTAAT 1218 CACCCACAACAAAAACTTTAATACCATTTGAATCCTAT------AAAGTT 1317 TTGTAACTGATAGACAAGTAACTCCCTTTTCCTAACATATACTTTACA 1377 AACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTATAGTCATATTTA 1557 ys-----AsnLysGluTyrGlyHisThrbeu 471 ||:::::::|| ||||||| || rphannetTyrasnThrTyrargLeuGluMetThrLeuThrValLeuAspLeuIle 293 ||:::||||||| ||||||::||| ysSerGluLeuIleArgGluValTyr---ThrAsnValAsnSerAspThrPheArg 326 |||||||::::: roTyraspilePheSerPheThrGlyasnGlnMetala------373 |||::: heThrHisThrAsnAspArgAsnIleIleTrpGlyAlaValHisGlyAsnIle 392 levalargHisArgGlu------TyrSerAsp 422 

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1087 CCCAATCTCGCTATAATGGAATATAAATTTAACACGTTCAGGGCTTAGATTATTTTCATTT 1146
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                                                                                                                                                                                                  367 AAAACAGTATGGACACAATTTATTAAAATGGGAGAAATTTTTGTTGATACACGTTAACA 426
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166 ProAsnSerThr-----AsnThrThrThrValArgGluArgPheGlnGluValAsn 182
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297 TyrAspProArgLeuTyrLysGluArgLeuSer------ValGluIleLeu 311
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ThrArgLysLeuTyrThrAspProileAsnTyrHisArgGlyIleSerLeuGluAlaAsp 331
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 44 TyrLysAspTrpThrAsnMetCysAlalleAspAsnAsnLeuLysSerlleAsnProPhe
                             GAGACATTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATTGTATCCGGT
                                                                                    247 ACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGAATAATAGGT
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| AlaGluLygTrpAsnLeuSerArgGlnGlyAspAspMet-------ProGly
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155 PheGluAsnAlaPheThrPheTrpIleAsn--------
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                                             2011 -----ACATTACCTTTAAATCGAAACATACCATTTATATTTAATCGTGCAGATGTA
                                                                                                  GlyGluAspThrLeuLeuMetThr------LeuTyrGlyThrProAsnHis
                                                                                                                                                          D OBVIX2 BACTV PRELIMINARY; PRT; 650 AA.
C 08VNX2;
C 08VNX2;
T 01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
T 01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
T 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
E Cry29Aa protein.
N Name=cry29Aa;
N Name=cry29Aa;
S Bacillus fuhuringiensis (subsp. medellin).
C Bacteria; Firmicutes; Bacillales; Bacillus (subsp. medellin).
C Bacteria; Firmicutes; Bacillales; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOLLECTION SACRETORY.

Dellectude A., Orduz S.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ251977; CAC80985.1; -; Genomic DNA.

GO; GO:0016787; F:receptor binding; IEA.

GO; GO:0005902; F:receptor binding; IEA.

GO; GO:0009405; F:pathogenseis! IEA.

GO; GO:0019435; F:spathogenseis! IEA.

InterPro; IPR005638; endotoxin_C.

InterPro; IPR005638; endotoxin_C.

InterPro; IPR005639; endotoxin_N.
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Pfam; PP00555; Endotoxin_M; 1.
Pfam; PF03945; Endotoxin_N; 1.
SEQUENCE 650 AA; 74435 MW;
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49.59%
32.38%
21.39%
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Best Local Similarity:
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Asn 675
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CryIVB(a)) (Crystaline entomocidal protoxin) (128 kDa
  2031
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                       1267 ACAGGTCCACCACAAAAACTTTAATACCATTTGAATCCTAT-----AAAGTTTCA 1320
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||IleThrGlnIleProAlaValLy9AlaTyrGlnLeuGlyValGlnSerGlnValIleLy8 501
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                                                          ----SerryrileAspLysvalPro
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P05519; P11782; P16479;
01-NOV-1988 (Rel. 09, Created)
30-MAY-2000 (Rel. 99, Last aquence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Pesticidial crystal protein cry4Ba (Insecticidal delta-endotoxin
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                  NUCLECTIDE SEQUENCE.
MEDLINE-88157738; PubMed-2831510;
Tungpradubtul S., Settasatien C., Panyim S.;
Tungpradubtul S., Settasatien C., Fanyim S.;
"The complete nucleotide sequence of a 130 kDa mosquito-larvicidal delte-endotoxin gene of Bacillus thuringiensis var. israelensis.";
Nucleic Acids Res. 16:1637-1638 (1988).
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Kloning and nucleotide sequences of the two 130 kDa insecticidal
protein genes of Bacillus thuringiensis var. israelensis.";
Agric. Biol. Chem. 52:873-878(1988).
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                                                             Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
WCBI_TaxID=1430;
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Name=cry4Ba; Synonyms=bt8, cryD2, cryIVB(a), isrH3;
Bacillus thuringiensis subsp. israelensis.
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EMBL; X05692; CAA29174.1; -; Genomic_DNA.

EMBL; D00247; BAA00178.1; -; Genomic_DNA.

EMBL; X07423; CAA30317.1; -; Genomic_DNA.

EMBL; X07423; CAA30312.1; -; Genomic_DNA.

PIR; S00399; USBSBI.
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MEDLINE=88185334; PubMed=2833395;
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InterPro; IPR001179; Bndotoxin.
InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin_N.
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Pfam; PP03944; Endotoxin_C; I.
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NUCLEOTIDE SEQUENCE.
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MEDLINE=22235415; PubMed=12324359;
DOI=10.1128/AEM.68.10.5082-5095.2002;
Berry C., O'Niel S., Ben-Dov B., Jones A.F., Murphy L., Quail M.A., Harris D., Zaritsky A., Parkhill J.;
"Complete sequence and organisation of pBtoxis, the toxin-coding plasmid of Bacillus thuringlensis subsp. israelensis.";
Appl. Environ. Microbiol. 6802-5095(2002).
ENGL; AL731882; CAD30095.1; -; Genomic DNN.
SEQUENCE 1136 AA; 127763 MW; 8AC4E8C26FE3E9B5 CRC64;
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10-MAY-2005 (TYENBLrel. 30, Last sequence update)
10-MAY-2005 (TYENBLrel. 30, Last annotation update)
10-MAY-2005 (TYENBLrel. 30, Last annotation update)
Pesticidial crystal protein cry4BA.
Name=cry4BA; Synonyms=BTB, cryD2, cryIVB(A), isrH3, pBt038;
Bacillus thuringiensis (subsp. israelensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
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Length:
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Mismatches:
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US-10-782-570-1 (1-2235) x Q8VNX1_BACTV (1-688)
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TTAGATGAACTTATATTTTATACAAAAATGAAACGTACGGGAAT------- 1191
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393 ValThrLysMetAspPheTyrLysIleAspGlyThrLeuAlaSerTyrAsnSerAsnIle 412
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LeuLysArgValAspPheTrpThr---AsnThrIleTyrGlnAspLeuArgPheLeuSer
                                                                                                                                                                                                                                                                     :::||| :::||| 340 AlaAsnLys1leGlyPheSerTyrThrAsnSerSerAlaMetGlnGluSerGly----
                                                                                                                                                                                                                                                                                                                                                                                                                                            377 AsnValTyrLysThrSerIle-------ThrAspThrSer----
                                                                              CCCAATCTCGCTATAATGGAATATAACTTTAACACGTTCAGGGCTTAGATTATTTCATTT
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CCAAGTACAGTAACATTACCTTTAAATCGAAAC----ATACCATTTATATTTAATCGT 2052
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                                                      ::: ||| :: ||| 595 AspalaileValProMetargLeuSerSerAsnGlnLeuIleThrIleAlaileGlnPro
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01-MAR-2002 (TEMBLrel. 20, Last sequence update)
01-MAR-2004 (TEMBLrel. 26, Last annotation update)
Cry30Aa protein.
Name=cry30Aa;
Bacillus thuringiensis (subsp. medellin).
Bacteria; Firmfuctes; Bacillales; Bacillus cereus group.
NOB_TAXID=79672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7E0D57085ED7B3A9 CRC64;
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NUCLECTIDE SEQUENCE.

Delecluse A., Orduz S.;

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ dat
EMBL; AJ51978; CAC80986.1; -; Genomic DNA.

GG; GO:0005102; F:receptor binding; IEA.

GG; GO:0005952; P:defense response; IEA.

GG; GO:00059465; P:pathogenesis; IEA.

GG; GO:0030435; P:pathogenesis; IEA.

R InterPro; IPR001178; Endotoxin.

R InterPro; IPR005539; endotoxin.

R Pfam; PF03944; Endotoxin.

R Pfam; PF03944; Endotoxin.

R Pfam; PF03955; Endotoxin.

R Pfam; PF03555; Endotoxin.

R Pfam; PF03555;
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Matches:
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949 ATCGCTCAATTTTCTTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGAATAGGT 1008
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       ATGAGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACT 948
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|SerSerIleAlaGly------IleSerAspMetThrPheTyrLysSerAspTyr 439
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                                                                                                                                                                                                  CAACAAGGIGCTGAATTGGCTGATGAATGGAATGCAGATATACATCCTTCACAAATTGAA
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|GlnArgGlyAlaValTyrGlyAspArgTrpGluLysAspIleAsnGlySer---IleSer
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                                                                                            PheAspSerValArgAspLysValIleAspLeuLysAsnAspTyrMetIleAsnProGlu
                                                                                                                               649 IATAAAACGCTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATTA
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129 GlnAspAlalleGlulleLeuValThrGlyValLysSerGlyTyrAsnAlaLeuLysAsn 148
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|GuTyrGluIleLeuAspAla----LeuProAsnTyrSerAsnMetValAsnAlaTyr 26
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                                                                                                                                                                                H., Asano S.;
databases.
                                             Bacillus thuringiesis (subsp. entomocidus).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
NCBI_TaxID=1436;
                                                                                                                                                                                                                                                                                                                                                                                                                              488B477B876BFDCA CRC64
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245
107
264
164
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     annotation update)
                                                                                                                                                                        Ikeyar T., Yamaya K., Ito T., Sahara K., Bando H., Submitted (OCT-2003) to the EMBL/GenBank/DDBJ dat. EMBL, AB125059; BAD00052.1; -; Genomic DNA. GO; GO:001679; Phydrolaee activity; IEA. GO; GO:000592; Pieferene response; IEA. GO; GO:0009405; P:pethogenesis; IEA. InterPro; IPR005639; endotoxin. C. InterPro; IPR005639; endotoxin. C. InterPro; IPR005639; endotoxin. N. Pfam; PP00945; Endotoxin. M. Pfam; PP00955; Endotoxin. M; I. Pfam; PP00955; Endotoxin. M; I. SEQUENCE 683 AA; 77438 MM; 48884778876BFDCA C.
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Matches:
Conservative:
Mismatches:
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05-JUL-2004 (TrEMBLrel. 27, L.
Putative mosquitocidal toxin.
Name=cry30Aa like;
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796.00
45.13%
31.41%
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598 AATGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAAACG 657
MISCELLANEOUS: Toxic segment of the protein is located in the
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HSSP; P07130; 1DLC.
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InterPro; IPR005639; endotoxin,C.
InterPro; IPR005639; endotoxin_N.
Pfam; PF03944; Endotoxin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                         1169 AA; 133544 MW;
                                                                                                                                                                                                                                                                                                                           Pfam; PP00555; Endotoxin_M; 1.
Pfam; PP03945; Endotoxin_N; 1.
Spornlation; Toxin.
SEQUENCE 1169 AA; 133544 MW
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IleLeuSerAspIleLysMetIleTyrPheArgThrGlyGlyMetTyrGlnValTyrAsp 502
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-!-FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
-!-FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
-!-FUNCTION: Promotes colloidosmotic lysis by binding scarabaeid beetles.
-!- DEVELOPMENTAL STACE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore cost.
                                                                                                                                                                                                    CCAGCAATCAAAGGTAACAGTCTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCAT
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|ProAlaValLysAlaLeuGlyIleSerThrAspSerLysValValLysGlyProValPhe
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---GluPheIleMetAspLysProSerIleAspValAlaIleArgGlyValGlnAsnAsp
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STRAIN=NREL B-18746 / PSSOC;
MIChaels T.B., Poncertada L., Narva K.B.;
Process for controlling scarab pests with Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Pesticidial crystal protein cry8Ba (Insecticidal delta-endotoxin CryVIIIB(a)) (Crystaline entomocidal protoxin) (134 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein).
Name-cry8Ba; Synonyms=50C(b), cryVIIIB(a);
Bacillus thuringiensis subsp. kumamotoensis.
Bacteria; Firmicutes; Bacillales; Bacillus;
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PheGlyTyrSerPhe--------
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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terminus.
SIMILARITY: Belongs to the delta endotoxin family.
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152
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QSW7N9;
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PheSerAsnTyrAspThrTyrProLeuala-------ThrThr 299
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AsnGlyAlaValLeuLeuAspIleValTyrProGlyTyrThrTyrThrPhePheGlyMet 431
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                                    CTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATACAACAAGGT 717
                                                                       ProPheLeuThrValTyrThrMetAlaAlaAsnLeuHisLeuLeuLeuLeuArgAspAla 214
                                                                                                            GCTGAATTGGCTGATGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCT 777
                                                                                                                                                                                    GGAACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATATATAGTAACTAT 837
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IleLeuAspSerLeuPheThrGlnTyrMetProSerPheArgValThrAsnPheGluVal 194
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SerllePheGlyGluGluTrpGlyLeu------SerThr
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                                        1654 AGAAATAATGCAATATCAGATAAAATAATTACAATGATCCCCAGCAATCAAAGGTAACAGT
                                                                                                                  CTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAGGAAACTTGGTTTAT
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EMBL; AB19814; BAD67157.1; -; Genomic_DNA.

GO; GO:0016102; F:receptor binding; IEA.

R GO; GO:0016952; P:defense response; IEA.

R GO; GO:0006952; P:defense response; IEA.

R GO; GO:0004045; P:sporulation; IEA.

InterPro; IPR005639; endotoxin.C.

InterPro; IPR005639; endotoxin.C.

InterPro; IPR005639; endotoxin.N.

Pfam; PF03944; Endotoxin.C; 1.

R Pfam; PF03944; Endotoxin.N; 1.
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Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
NCBI_TaxID=1428;
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Last annotation update)
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res: 9.45e-43 Length: 688 755.50 Matches: 241 arity: 46.42\$ Conservative: 109 nilarity: 31.96\$ Mismatches: 275 2 Gaps: 33	-1 (1-2235) x QSW7N9_BACTU (1-688)	aataataatgaatatgagattatcgattcaagaatttatcttatccttctaacagaat 72              :::  SerababgserglulleleuabalaserSerababserabmetser 23	AITGAICAITCIAGAIACCCITACACAAAITAATCCAAATCAACCAITACAAAACACAAAT 132	:       sTyrProLeuAlaHisSerArgGlnAspSerMetG	Tacaaagagtggctcaatatgtgtcaagggaatacacaatatggtgataatttggagaca 192                       TyrLygGluttpIleaenGlnCyeGluthrIleaenthr 56	AATTGCTGCAGTTAGTGCAGGTACTATTGTATCGGT 2	Prolleaspinraspileasnservalalaarainrilesiyalauy /e	ACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCCGACCGA	NATCTTTTGGTACCCTAATC	PhevalLeuSerThrPheThrSerLeuIleProTyrLeuTrpProSerAspThr 108	A 4	LysLysllefrpGlyAspPheThrLysGlnGlyLeuGlnLeuPheArgProGluLeuGly 128	46	AsnaspalaileGluIleIleGlyAsnAspValGlnSerGluTyrAsnSerLeuLysThr 148	AGACAAATATTACAAAGCTATAATACAGCATTAGATGATGAGAAAAATTAAAAAGA 52	PheMetGlnAsnPheGluAspSerPheThrAspTrpLysLysLysTyrAtgAsn 165 CTACAAGCTCCTGGATTACCACCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAA 585	17	IGITCACAATGATTTATTCGAGAAATACCTGGTTTCCAAC	AsnAspPheSerSerValArgAspGlnIleIleArgLeuLysAspArgPheLeulleAsn 193	ACTIATAAAACGCTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAAT 702	ProGluAsnLysProAlaPheLeuIleLeuTyrAlaGlnThrAlaAsnPheAspLeuIle 213	TTATTACAACAAGGTGCTGAATTGGCTGATGGAATGGAA	LeuTyrdinargdiyalaLeuTyralaaspGluTrpGluAsnaspIleAs	AITGAACCTAATGCTGGAACATCAGATGACTATTATAAACTITTTAAAAGAAAATATACCT 8		AAATATAGTAACTATTGTGCAAATACCTATAGAGAAGGACTAAATAAA	
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è 8	326 GluSerAenTyrPheGlu	GINSERABITY PREGINSerLeuglugly Leugluhen ale a 122 de 122 d
à	1123 TCAGGGCTTAGATTATTTTCATTT	TCAGGGCTTAGATTATTTTCATTTTTAGATGAACTTATATTTTTATACAAAAATGAAACG 1182
QQ	343 ProProSerLeuPheThrTrpl	oleuangluleuanlyrihrileargoluan 361
ð í	1183 TACGGGAATCGTTTAGTTGGTATT	
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දු පු	1207 GCGAATCGTAATAGATCTACTTATY	GCGAATCGTAATAGATCTATATGCTACGACAGGAACTGAAATTATATATA
ò	1267 ACAGGTCCACCCACAAAAACT	ACAGGICCACCACAAAAAACTITAAIACCAITIGAAICCIAIAAGIIIICAAIIGIA 1326
q	396 AsnGlyThrProThrGlnIleGly	
È	1327 ACTGATAGACAAGTAACTCCTACTTCCCCTTTT	CCTAACATATACTTTACAATT 13
gg G	415	-SerGlnTyrHisHisProAsnGluCysTyrSerile 426
ò	1381 AATCAAATT	TTATTTAAATAATTCACCTAGTAAT
qq	427 AlaGlyileSerAspMetThrPhe	elyrLysSerAspfyrAsnGlyAsnAlaProThrThr 446
à	1420 AAATTAACATATTCAGCTGGGGGG	AAATTAACATATTCACCTGGGGGGAATTTATCTAATGATAAAAAAACAACTGATTTTCAA 1479 :::
qq	447 GlnthrtyrGlnAlaGlyArg	46
È	1480 TTTCCTGTAAAAAAAGACTGTAAA	TITICCIGIAAAAAAGACTGIAAACCAATIAITAATCCAAATIGITAACCAAGCTATAAT 1539
g	465 GlyProGlnGluAlaSerSerSer	47
& 8	1540 AGTTATAGTCATATTTTATCCCAG :::          479 GlnThraenHisIleLeuSeraep	AGTIATAGTCATATTTTATCCCAGTTTTCTTTATTTAATTATTCCTATAAATTGGATTA 1599 :::
à	1600 GCGCTAAATATATATATACAGGT	rgcartaggarggrcacagrafigrrtaatagaaat 1659
qq	::: 498 TyrProSerTyrAspPheGlyTyr	TyrproserTyrAspPheGlyTyrSerPheAlaTrpThrHisThrSerValAsnProAsp 517
È	1660 AATGCAATATCAGATAAATTAATT	AATGCAATATCAGATAAAATAAAAAGATCCCAGCAATCAAAGGTAACAGTCTTGAT 1719
QG QG	518 AsnieuileValProAsnArgile	ethrginileproAlavaliysAlaAspTyrLeuthr 537
ò	0	ACBARCTCTBAGGTABITGAAGGCCTGGTCATACAGGAAGAAACTTGGTTTATTA 1776
e G	538 SerProAlaLysValileAlaGly	
à	1777CAAAGTCAAGGGCGT	CAAAGTCAAGGGGTTTAGAGATTACATGTAGAACTCCTAATTCTACA 1824
qq	558 AsnalaalaThrGlnAladlyArg	gMetGlnileGlnCysLysThrGlySerPheThrGly 577
š	1825CAATCTTATTACATTAGA	ACTICGATACGCTACAAATGGTGCT 1866
QQ Q	578 AlaSerArgArgTyrGlyileArg	rargargiyrdlyileArgileArgiyrAlaAlaAshAsnAlaLeuThrValSer 597
ò	1867GGA	CAGGA 19
Op	598 LeuSerTyrThrValGlnGlyĠly	yAsırhrMetSerThrThrPheIleThrGluArgThr 617

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GTAATAGGAATACCACCTCAACGACTCAACAACACTTTTTCTGGTACAAATTATAATA 1965
                                                                                                                                                                                                         649 GlnAsnThrIleValThrIleAlaIleGlnGlnLeuAsnAlaPheProAsnAspGlnLeu 668
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WUCLINE-99369730; PubMed-9704107;

Hwang S.H., Saitoh H., Mizuki E., Higuchi K., Ohba M.;

Hwang S.H., Saitoh H., Mizuki E., Higuchi K., Ohba M.;

Hwang S.H., Saitoh H., Mizuki E., Higuchi K., Ohba M.;

A novel class of mosquitocidal delta-endotcoxin, Cry198, encoded by a Bacillus thurings of ensist source gene.";

Syst. Appl. Microbiol. 21:179-184 (1998).

-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of mosquitos.

-!- DEVELOPMENTAL STARE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                        618 Pheteu------ThrasprokanAhrilePro-----Thrasp
                                                                                  ACAGTAACATTACCT
                                                                                                                                                                  TTAAATCGAAACATACCATTTATATTTTAATCGTGCAGATGTA---TCAAATTCAATTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the spore coat. MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Pesticidial crystal protein cry19Ba (Insecticidal delta-endotoxin CryXIXB(a)) (Crystaline entomocidal protoxin) (78 kDa crystal
                                                                                                                                                                                                                                                    2077 ATCATTGATAAATTGAATTTATACCAATTACTTCCTCTGTA 2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus,
                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5351EA63E2B042F7 CRC64;
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                                                                                  TTACAATACGGAGATTTTGGGTATTTCCAATTTCCAAGT----
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                              682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; Q06117; 1JJG.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
Pfam; PP03944; Endotoxin.C; 1.
Pfam; PP03945; Endotoxin.M; 1.
Pfam; PP03945; Endotoxin.M; 1.
Plasmid; Sporulation; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus thuringiensis subsp. higo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein).
Name=cry19Ba; Synonyms=cryXIXB(a);
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NCBI_TaxID=132266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 AGCATAAAACAGCTAAAGTTACAAACTTTAGAAGGATTTAGACAAATATTACAAAGCTAT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 AspThrLeuAsnArgAlaThrSerAsnLeuSerGlyLeuAsnGluSerLeuAsnIleTyr 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GluLeuIleArgSerTyrIleAsnAspLeuHisIle 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATTGTGCAAATACCTATAGAGAAGGACTAAAATAAACTTCGAAACGAACCTAATATGAGA 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrCysValAsnThrTyrLysSerGly------LeuGluSerLysLysGlnIleGly 254
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US-10-782-570-1 (1-2235) x C19BA_BACUH (1-682)
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                    CTIGAAAITCAACCCAAICTCGCIAIA-----AIGGAAIAIAATTIAACACGIICAGGG 1128
                                                            CTTAGATTATTTTCATTTTTAGATGAACTTATATTTTATACAAAAATGAAACGTACGGG 1188
                                                                                                                                          249 ATTATATATAT------GGAGAAAGAAGAACAGGTCCACCACAAAAAACTTTA 1293
                                                                                                                                                                                                                             ACTCCT---ACTTCCCCT-----TTTCCTAACATATACTTTACAATTAATCAATTGAA 1392
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LysAlaGluLeuThrArgGluIleTyrSerAspValIleAsn---AspHisValTyrGly 312
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                                                                        |||| ::::::|||
---HisAlaPheThrTrpLeuLysGlyPheArgPheValThrAsnSerIleAsnSerTrp
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LeuMetVal---ProTyrIleSerPheGluHiBAlaGluSerLeuTyrThrArgArgPro
                                                                                                    AATCGTTTAGTTGGTATTGCGAATCGTAATAGATCTACTTATGCTACGACAGGAACTGAA
                                                                                                                       351 ThrPheLeuSerdlyGlyGluAsnArg-----TyrPheLeuThrHisGlyGluGly
                                                                                                                                                                                    ATACCATTTGAATCC------TATAAAGTTTCAATTGTAACTGATAGACAAGTA
                                                                                                                                                                                                                                                 408 TyrproTrpThrAgpProvalAsnIleThrLysileAsnPheSerileThr-----
                                                                                                                                                                                                                                                                                                                                LysProThrValArgThrAspPheAsnPheLeuLeuAsnArg--------
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                                                                                     din------AladinGlyTyrAspThrTyrAspGlnAsnAlaAsnGlyMetTyrHis 659
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                                                                                                                                    Crystal protein Cry9Dbl.
Name=cry9Dbl;
Name=cry9Dbl;
Bacillus thuringiensis.
Bacteris; Firmicutes; Bacillales; Bacillus cereus group.
Name=cry9Dbl;
Bacillus cereus group.
                                                                                                                                                                                                                                                                                                                                                                                                                    Flannagan R.D., Abad A.R.;
"Bacillus Cry9 Family Members ";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AY971349; AAX78439.1; -; Genomic DNA.
SEQUENCE 1169 AA; 132126 WW; 85DCOED5083E3P43 CRC64;
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Q56B08;
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ò	TyrTrp11eG GGAACTGAAA	380
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අ දි		360
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. a	AATCTCGCTATAATGGAATATAATTTAACGCTTCAGGGCTTAGATTATTTCATTTTTA	1090
ය දි	GluSerPheTyrAsnIleArgAlaAlaArgGluArgLeuThrPheSerGlnLeuGlu 346	328
ය දි 	::        GluValTyrThrAspProlleValPheAsnProProGluProProSerGlyAlaPheCys	308
ò		294
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	3 TATCGAAGAIATATGACTATTACTGTATTAGATACTATCGCTCAATTTTCTTTTTATGAT 972                  :::    :::    :::	913
3 A 8	3 AGAGAAGGACTAAATAAACTTCGAAACGAACCTAATATGAGATGGAGTATATTTAATGAT 912 	853
3 8 8	3 TATTATAAACTTTTAAAAGAAAATATACCTAAATATAGTAACTATTGTGCAAATACCTAT 852 ::::::	793
3 A 8	3 GAATGGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCTGGAACATCAGATGAC 792 	733
5 A 8	3 TATGCGCAAGCTGCTAATTTTCATTTAATATTATACAACAAGGTGCTGAATTGGCTGAT 732 	673
3 A &	S ATACCTGGTTTCCAACTTGAAACTTATAAAAGCTATTACTACCTATT 672 :::	625
3 A 8	5 CAAGCTGCCTTGACTCTTAAAATACGATTTGAGAATGTTCACAATGATTTTATTCGAGAA 624 	565
S 8 8	S GATTGGAGAAAATTAAAAGACTACAAGCTCCTGGATTACCACCATCATCAGCATTACAA 564 	505
S 8 8	5 AAGTTACAAACTTTAGAAGGATTTAGACAAATATTACAAAGCTATAATACAGCATTAGAT 504 	135
a 8	<pre>5 TTTATTAAATGGGAGAATTTTGTTGATACAGGTAACAGAAAGCATAAACAGCTA 444</pre>	385 115

aarch completed: January 12, 2006, 06:34:38 bb time : 290.5 secs Bacillus Bacillus B.t. toxi Dipteran crylOAa. Bacillus

Bacillus cry4Ba. 1 Bacillus

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Bacillus BtPGS1208 Antiscara Amino aci cry3Ba. 1

Amino aci Bacillus Bacillus

Minimum DB Maximum DB

OM nucleic

Run on:

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delta-endotoxin; delta-endotoxin associate polypeptide;
expression cassette; transformation; transgenic; plant; bacteria;
lepidoptera; coleoptera; pest; pesticide; resistance;
pesticidal activity.
        Adf31302

Adf31307

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; 2003US-044863P.
; 2003US-044879P.
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Bacillus thuringiensis
Misc-difference
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 -MONDEL-frame+ n2p.model -DEV=xlp
-MODEL-frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO epool_p/US10782570/runat_12012006_060221_7509/app_query.fasta_1.2375
-Q=/cgn2_1/USPTO epool_p/US10782570/runat_12012006_060221_7509/app_query.fasta_1.2375
-DB=A_Geneeq_-QFMT=fastan -SUPFIX=xag -MINMATCH=0.1_LOFQTCL=0.LOFQTCR=0
-DGALIGN=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=+5
-DOCALIGN=D0 -TRR SCORE-pct -TRR MAX=100 -TRR MIN=0 -ALIGN=15 -MODE=LOCAL
-USTRENT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USTRENT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-NORMSTS-70 GGGN 11 260 GAUNAT -12012006 G60221 -7509 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPFOP=10 -YGAPEXT=0.5 -DBLOEN=7
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Adr89395 AXM1-007
Adr89395 AXM1-006.
Adr893715 Delta-end
Adr89426 cry44a.
Aap94035 Delta-end
Aap8439 Insectici
Aar14373 Dipteran
Aar14373 Dipteran
Aar63078 B.t. toxi
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         GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                              - protein search, using frame_plus_n2p model
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                                                                                                                                                                                   This sequence represents an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide realstance, specifically bacteria and plants. These organisms are useful for sensiting altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or organisms.
                                                                                                                              New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.
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       19-PEB-2004; 2004US-007B2020.
19-PEB-2004; 2004US-007B2196.
19-PEB-2004; 2004US-007B2141.
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1020 1080 1140 1200 1260 1320 1380 1440 1500 480 180 160 540 900 200 9 220 720 240 780 840 280 360 380 400 420 440 460 480 GlnAspLysThrValTrpThrGlnPheIleLysMetGlyGluIlePheValAspThrPro 140 260 900 960 500 LeuProProSerSerAlaLeuGlnGlnAlaAlaLeuThrLeuLysIleArgPheGluAsn GInSerTyraanThralaLeuAapaapTrpArgLysLeuLysArgLeuGlnAlaProGly TTACCACCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAGAAT ValHisAsnAspPheIleArgGluIleProGlyPheGlnLeuGluThrTyrLysThrLeu GAATTGGCTGATGGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCTGGA ThrSerAspAspTyrTyrLysLeuLeuLysGluAsnIleProLysTyrSerAsnTyrCys TTAACAGAAAGCATAAAACAGCTAAAAGTTACAAACTTTAGAAGGATTTAGACAAATATTA CAAAGCTATAATACAGCATTAGATGGATGGAGAAAATTAAAAAGACTACAAGCTCCTGGA GTTCACAATGATTTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTTATAAAACGCTA ACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATATAGTAACTATTGT TCTTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGCATTAAAACT GCAAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACCTAATATGAGATGGAGT ATAITTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACTATCGCTCAATTT TCATTITIAGATGAACTIATATITIATACAAAAATGAAACGTACGGAATCGTTTAGTT ATTGTAACTGATAGACAAGTAACTCCCTACTTCCCCTTTTCCTAACATATACAATT 1381 AATCAAATTGAACTTTATTTAAATAATTCACCTAGTAATAAATTAACATTTCAGCTGGG 481 ઠ

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                                                                                                                                                                                                                                                  CCTCAACGACTCAACAACACTTTTTCTGGTACAAATTATAATAATTACAATACGGAGAT
                                                                                                                                                                                                                                                             ProglnArgLeuAsnAsnThrPheSerGlyThrAsnTyrAsnAsnLeuGlnTyrGlyAsp
                                                                                                                                                                                                                                                                                                ATATTTAATCGFGCAGATGTATCAAATTCAATTTTAATCATTGATAAATTGAATTTATA
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AAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTATAGTCATATTTTATCC
                                                                                                         ATTACAATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAAACTCTAAGGTAATTGAA
                                                                                                                                          GGACCTGGTCATACAGGAGGAACTTGGTTTATTTTACAAAGTCAAGGGCGTTTAGAGATT
                                                                                                                                                                             ACATGTAGAACTCCTAATTCTACACAATCTTATTACATTAGACTTCGATACGCTACAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           delta-endotoxin, delta-endotoxin associate polypeptide;
expression cassette; transformation, transgenic; plant; bacteria;
lepidoptera; coleoptera; pest; pesticide; resistance;
pesticidal activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADR89399 standard; protein; 694 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AXMI-007 alternative protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus thuringiensis.
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This sequence represents an isolated delta-endotoxin. Some of the delta-
endotoxin coding sequences of the invention have alternative start
codons, producing more than one protein from a single open reading frame.
The nucleic acid sequences of the invention are useful in DNA constructs
or expression cassettes for transformation and expression in plants and
bacteria. The nucleic acids and corresponding polypeptides are useful for
Killing lepidoperan or coleoperan pests. Compositions containing the
CK climing lepidoperan of organisms with pesticide resistance,
useful for the production of organisms with pesticide resistance,
specifically bacteria and plants. These organisms are useful for
generating altered or improved delta-endotoxin or delta-endotoxin.

Sesociated proteins that have pesticidal activity, or for detecting the
presence of delta-endotoxin or delta-endotoxin-associated proteins or
nucleic acids in products or organisms.
                                                                                                                                                                                                                                                                                                                                                          isolated delta-endotoxin and delta-endotoxin-associated nucleic acids polypeptides, useful for killing lepidopteran or coleopteran pests or producing organisms with pesticide resistance.
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Conservative:
Mismatches:
Indels:
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                                                    20-FEB-2003; 2003US-0448633F.
20-FEB-2003; 2003US-0448797F.
20-FEB-2003; 2003US-044810F.
20-FEB-2003; 2003US-0448812P.
19-FEB-2004; 2004US-007812P.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-00782096.
19-FEB-2004; 2004US-00782141.
19-FEB-2004; 2004US-00782141.
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Percent Similarity:
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                20-FBB-2004;
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391 AAAATGGGAGAAATTTTTGTTGATACACCGTTAACAGAAAGCATAAAACAGCTAAAGTTA 450

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441 AspPheGlnPheProValLysLysAspCysLysProllelleAsnProAsnCysLeuPro 46	Qy 1531 AGCINIDATHATHAGTCAINTTTATCCCAGTTTTCTTTATTTATTCTATTATTCCTAINA 1590	Qy         1591 ATTGGATTAGGGCTAAATATATATATAGGGGGATTAGGATGGACACACAGTAGTGTT 1650           Db         481 IleGlyLeuAlaLeuAsnIleLeuTyrThrdlyAlaLeuGlyTrpThrHisserSerVal 500	Qy 1651 AATAGAAATAATGCAATATCAGATAAATAATTACAATGATCCCAGCAATCAAAGGTAAC 1710	Oy 1711 AGTCTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAGAACTTGGTT 1770	1771	Qy 1831 TATTACATTAGACTTCGATACGCTACAAATGGTGGTGGAAATACTCCTAATATATCT 1890	1891	Qy 1951 ACAAATTATAATAATTACAATACGGAGATTTTGGGTATTTCCAATTTCCAAGTACAGTA 2010	Qy 2011 ACATTACCTTTAAATCGAAACATATCTTAATCGTGCAGATGTATCAAATTCA 2070	Qy 2071 AITTTAATCAIGATAAAATTGAAATTTATACCAATTACTCTCTGTACGCCAAAATAGA 2130	Oy 2131 GAAAAACAAAAATTAGAAACTATCCAAAAAAATAAATACATTTTTCACAAATACA 2190 	Qy 2191 AAAATACTTTAAATAGAAGCCACAAACTATGATTGAT 2232 	RESULT 3 ADR89395 ID ADR89395 standard; protein; 735 AA.	AC ADR89395; XX DT 18-NOV-2004 (first entry)		KW delta-endotoxin; delta-endotoxin associate polypeptide; KW expression cassette; transformation; transgenic; plant; bacteria; KW lepidoptera; coleoptera; pest; pesticide; resistance;		PN WO2004074462-A2. XX PD 02-SRP-2004	20-FEB
	451 CAAACTTTAGAAGGATTTAGACAAATATTACAAAGCTATAATACAGGATTAGG 510 	57	GCCTTGACTCTTAAAATACGATTTGAGAATCACAATGATTTTATTCGAGAATACCT	GOTTICCAACTTGAAACTTATAAAACGCTATTACTACCTATTTGGGGAAGCTGCTAAT	ATATA        spile	751 CATCCTTCACAAATTGAACCTAATGCTGGAACATCAGATGACTATTATAAACTTTTAAAA 810 	GAAAATATACCTAAATATAGTAACTATTGTGGAAATACCTATAGAGAGGACTAAATAAA		ATTACTGTATTAGATACTATACGTCTATTTTTTTTTTTT	TCAATAGGAAGAATAGGCATTAAAACTGAACTTACAAGAAAATTATACAACTGA 	ATAAATTTTGACGTCTTACCTTGAAATTCAACGCATCTCGCTATAAATATTTTGACGTCTTACTTGAAATTTTAAATTTTGACGTTATATTTTTATTTA	AATTTAACACGTTCAGGCTTAGATTATTTTCATTTTTAGATGAACTTATATTTTAGATGAACTTATATTTTAGATACAATTTTAGATACAATTTTAGATGAACTTATATATTTAGATAGA	1171 AAAATGAAACGTACGGAATCGTTTAGTTGCGAATCGTAATAGATCTACTTAT 1230 	GCTACGACAGGAACTGAAATTATATATGGAGAAAGAACAGGTCCACCACACAACAAAACT	alanii iiilolyiiilolalalalalalalalalalalalalalalalalal	LeulleProPheGluSerTyrLysValSerIleValThrAspArgGlnValThrProThr	1351 TCCCTTTTCTAACATATACAATTAATCAAATTGAACTTTATTTA	1411 CCTAGTAATAAATTAACATATTCAGCTGGGGGGAATTTATCTAATGATAAAAAAACAACT 1470 	GATTITCAATTICCTGTAAAAAGACTGTAAACCAATTATTAATCCAAATTGTTTACCA

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                                                            GluGinAspiysThrValTrpThrGlnPheileLysMetGlyGluIlePheValAspThr
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               TTACAAAGCTATAATACAGCATTAGATGATTGGAGAAAATTAAAAAGACTACAGCCCT
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                                               gaacaagacaaaacagtatggacacaatttaattaaaattgggagaaatttttgttgataca
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20-FEB-2003; 2003US-0448632P.
20-FEB-2003; 2003US-0448633P.
20-FEB-2003; 2003US-0448863P.
20-FEB-2003; 2003US-0448810P.
20-FEB-2004; 2003US-0448810P.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-00782191.
19-FEB-2004; 2004US-00782191.
19-FEB-2004; 2004US-00782191.
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ATTTATCCCAGTTTTCTTTATTTAATTATTCCTATAAAATTGGGATTAGCGCTAAATATA
                                                                                    VallleGluGlyProdlyHisThrGlyGlyAsnLeuValTyrLeuGlnSerGlnGlyArg
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The 130 kDa delta-endotoxin from B. thuringiensis subsp. israelensisis is encoded by a 4.46 kb insert of pCH130. The protein is insecticital and can be used to control insert pests esp. mosquitos. See also AAP94035. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to
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AsnLysAsnGluTyrGluThrLeuAsnAlaSerGlnLysLysLeuAsnIleSerAsnAsn
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                                                                                                                      DNA fragment encoding insecticidal protein - obtd. from Bacillus
thuringiensis sub species israelensis, and used in microorganisms and
plant cells.
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                                            TTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTTACAACAAGGTGCT 720
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CCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAGAATGTTCAC
                                                                                                                                                                ProGluLeuValAsnSerCysProProAsnProSerAspCysAspTyrTyrAsnIleLeu
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LysPheGluAlaTyrLeuLysAsnAsnAsnArgGlnPheAspTyrLeuGluPro---LeuPro
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375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn
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394 IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu
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lepidoptera; coleoptera; pest; pesticide; resistance;
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                                                                                                                                                                                                                                                                                                                                                 isolated delta-endotoxin and delta-endotoxin-associated nucleic acids polypeptides, useful for killing lepidopteran or coleopteran pests or producing organisms with pesticide resistance.
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LysPheGluAlaTyrLeuLysAsnAsnAsGlnPheAspTyrLeuGluPro---LeuPro 265 ValThrThrTyrLysLysGlyLeuAsnLeu1leLysThrThrProAspSerAsnLeuAsp ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr 394 IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu 1294 ATACCATTIGAATCCTATAAAGTTTCAATTGTAACTGATAGACAAGTAACTCCTACTTCC -----GlyLeuAlaThrAsnIleTyrilePheLeuLeuAsnValIleSerLeuAspAsn CCATCATCACCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAGAATGTTCAC TTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTTATTACAACAAGGTGCT GAATTGGCTGATGAATGGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCTGGA ---AATATGAGATGAGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTA |||| :::||| ||| ||| |||| AspleuvalalaleupheProAsnTyrAspValGlyLysTyrProlle-----1063 CGTCTTACTTTACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAATTTAACACGT CCTTTTCCTAACATATACAATTAATCAAATTGAACTTTAATTTAAATTCACCT GAAAGCATAAAACAGCTAAAGTTACAAACTTTAGAAGGATTTAGACAAATATTACAAAGC TATAATACAGCATTAGATGATTGGAGAAAATTAAAAAGACTACAAGCTCCTGGATTACCA AATGATTTTATTCGAGAAATACCT-----GGTTTCCAACTTGAAACTTATAAAACGCTA 781 ACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATATAGTAACTATTGT GCAAATACCTATAGAGGACTAAATAAACTTCGAAACGAACCT 427 151 547 607 186 199 206 721 226 841 943 305 1003 321 338 356 414

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GlyAspLeuIle-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn
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                                                                                                                                                                                                                                                                                                                                                                    toxin; crystal protein; insecticide; pCC130; control agent.
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The protein is encoded by an insert in plasmid pCC130. The delta endotoxin protein is insecticidal and can be used to control insect pests esp; meaquitos. See also AAP93715. (Updated on 25-MAR-2003 to correct PAfield.) (Updated on 25-MAR-2003 to correct DR field.) (Updated on 27-MUG-2003 to correct OS field.)
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                             A plasmid contg. the gene is isolated by forming a gene library from plasmid DNA of B.thuringtensis israelensis (HD 522 strain, USA Goldberg ONRGO) followed by screening with anti-israelensis insecticidal protein IG. The insecticidal protein is highly effective against Diptera, esp. Aedes. See also AAP81034. (Updated on 24-OCT-2003 to standardise OS
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|TyrHisAsnHisLeuLysThrTrpGlu------AsnAsnProAsnProGln
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AAR14374. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-
AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCACAAATCATACAAAAAATACTTTAAATATAGAAGCCACAAACTATGATATTGAT 2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::: ||| ||| ||||||||| TyralaasnProlleLysasnThrLeuGlnSerGluLeuThraspTyraspIleasp 719
                                                                                                                       PheGlnGlnSerTyrPheIleArgIleArgTyrAlaSerAsnGlySerAlaAsnThrArg
                                                                                                                                                                                                 ThrPheSerGlyThrAspTyrThrAsnLeuLysTyrLysAspPheGlnTyrLeuGluPhe
                                                                                                                                                                                                                                                                             TCTACACAATCTTACATTAGACTTCGATACGCTACAAATGGTGCTGGAAATACTCTT
                                                                                              CCTAATATATATCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAACAAC
                                                                                                                                                                             ACTITITICIGGTACAAATTATAAAAATTAACAATACGGAGATTTTGGGTATTTCCAATTT
                                                                                                                                                                                                                                                                                                                                     GTA---TCAAATTCAATTTTAATCATTGATAAAATTGAATTTATACCAATTACTTCCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence was deduced from the DNA sequence obtd. from plasmid
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166 ABnThrGlnAspValArgThrGlnIleGlnLeuValHisTyrHisPheGlnAsnValIle
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LysPheGlualaTyrLeuLysAsnAsnArgGlnPheAspTyrLeuGluPro---LeuPro
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Length:
Matches:
Conservative:
Mismatches:
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2176 TICACAAATCATACAAAAATACTTTAAATATAGAAGCCACAAACTATGATATTGAT 2232
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Matches:
Conservative:
Mismatches:
Indels:
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-067338/09.
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACAGTAGTGTTAATAGAAATAATGCAATATCAGATAAAAAAATAATTACAATGATCCCAGCA 1698
                                                        GATACTATCGCTCAATTTTTCTTTATGATATAAGAGATACAAAGATTCAATAGGAAGA 1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                   471 LyshanilephedlyLeuproileLeuLysProArgGluAsnGlnAlaileProThrLeu 490
                   ---AATATGAGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTA 942
                            ValThrThrTyrLysLysGlyLeuAsnLeuIleLysThrThrProAspSerAsnLeuAsp 284
                                                                                                                                                                                                                                                                                                                                                1123 TCAGGGCTTAGATTATTTTCATTTTAGATGAACTTATATTTTATACAAAAAATGAAACG
                                                                                                                                                                                     375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn
                                                                                                                                                                                                                                                                   1414 -----AGTAATAAATTAACATATCAGCTGGGGGAATTTATCTAATGATAAAAA
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|HisSerSerValAspProLysAsnThrileTyrThrHisLeuThrThrGlnIleProAla
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                                                                                               1003 ATAGGTGGCATTAAAACTGAACTTACAAGAGAAATTTATACAACTGAAATTTTTGAC
                                                                                                                                    1063 CGTCTTACTTACCTTGAAATTCAACCCAATCTCGCTATAAATGGAATATAATTTAACACGT
                                                                                                                                                        338 GluSerProTyrLysTyrTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg
                                                                                                                                                                                                                                                        1234 ACGACAGGAACTGAAATTATATATGGAGAAAGAACAGGTCCACCACCACAAAAACTTTA
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A library was constructed from Bacillus thuringiensis PS71M3 total cellular DNA in lambda Gem-11. Plasmid pMYC1625, selected in Escherichia coli, contained a 8.0 kb insert expressing a beta-endotoxin gene. This was sequenced (AAQ81178). A cured, acrystalliferous B.t. host carrying pMYC1625 produced a 130 kb acrystal protein (AAA63078) toxic to calliphorids. (Updated on 25-MAR-2003 to correct PN field.)
Delta-endotoxin; crystal protein; biological control agent; Calliphorid; screw-worm; sheep blowfly; Lucilla; Phormia; Calliphora; insecticide; pesticide; B.t.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method for controlling Calliphoridae pests - specifically utilises Bacillus thuringiensis isolates or toxins.
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282
131
282
64
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Conservative: Mismatches: Indels:

901.00 49.29% 34.19% 22.87%

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US-10-782-570-1 (1-2235) x AAE26353 (1-1109)
         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                          661 ValTyrThrAsnThrThrValLeuIleAspLysIleGluPheLeuProIleThrArgSer 680
                                                                           ITCACAAATCATACAAAAATACTITTAAATATAGAAGCCACAAACTATGATATTGAT 2232
                                                                                        ::: ||| |||||||||||| || TyralaAsnProlleLysAsnThrLeuGlnSerGluLeuThrAspTyrAspIleAsp 719
                                       Novel isolated delta-endotoxin nucleic acid molecules, cry26Aal and cry28Aal isolated from Bacillus thuringiensis finitimus, that encodes toxin active against insects, useful for controlling insects.
                                                                                                                                                                                                                                                      Delta-endotóxin, cry26Aal; cry28Aal; insect-resistant plant; toxin;
transgenic host cell; insecticide.
                                                                                                                                                                                                                              Bacillus thuringiensis ssp. finitimus cry28Aa1 delta-endotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JA, Lewitin EI, Zalunin IA, Revina LP;
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                                                                                                                                                      AAE26353 standard; protein; 1109 AA
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ZALUNIN I A.
REVINA L P.
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N-PSDB; AAD43974.
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Chestukhina GG;
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1109

Length:

6.49e-67

Alignment Scores: Pred. No.:

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199 AGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATTGTATCCGGTACTCTGTTAGCC 258
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LysGlulleAlaLeuAlaH1sLeuAsnGlyPheLysAspValLeuThrTyrTyrGluArg 120
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266 ArgArgPhePro-------ArgGlyValGluLeuGluLeuThrArgGlu
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                                                                                                                                  336 Asn------ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly 350
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                                               508 LystyrAlaileSerLeuPheTyrAlaAlaAsnAsnAlaIleAlaValSerIleAspVal
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619 AsnValLeuPhelleAsnAlaThr --- AsnAlaLeuLysMetAspValThrAspTyrHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid molecule encoding a toxin that is active against insects useful for controlling insect pests or for conferring insect resistance in plants.
                                                                                                                                                                                                                                                                                                                                                                               Bacillus thuringiensis serovar finitimus cry28Aa1 delta-endotoxin.
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transgenic plant; insect resistance; insecticide.
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                                                                                                                                                                                                                     ADF31302 standard; protein; 1109 AA
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976 AAGAGATACAAAGATTCAATAGGAAGAATAGGTGGCATTAAAACTGAACTTACAAGAGAA 1035
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LysGluIleAlaLeuAlaHisLeuAsnGlyPheLysAspValLeuThrTyrTyrGluArg
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LysGlyLeuAsnHisLeuLysGluSerGluLysIleThrTrpAspAlaTyrAsnThrTyr
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300 IleGluLeuTyrThrGluSerValAlaGluGlyABpTyrLeuSerGlyIle-----
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                                                          GCATTAGATGATTGGAGAAAATTAAAAAGACTACAAGCTCCTGGATTACCACCATCATCA
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266 ArgArgPhePro------ArgGlyValGluLeuGluLeuThrArgGlu
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|SerSerAspThrValAlavalValSerAlaGlyIleValValValValGlyThrIleLeuThr 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  delta-endotoxin nucleic acid molecules, cry26Aa1 and cry28Aa1, controlling insect pests and for conferring insect resistance.
                                 Bacillus thuringiensis serovar finitimus cry28Aal delta-endotoxin.
                                                                      Cry26Aal; cry28Aal; delta-endotoxin; insect pest control.
transgenic plant; insect resistance; insecticide.
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LEWITIN B I.
ZALUNIN I A.
REVINA L P.
CHESTURHINA G G.
(first entry)
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                                                                                            TyrgluVal---ThrAsnAsnSerVallleArgGlyProGlyPheThrGlyGlyAspLeu 490
------ProAsnAspTyrGlyGly 413
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                                                          GTTAATAGAAATAATGCAATATCAGATAAAAATAATTACAATGATCCCGGCAATCAAGGT
                                                                                                                                                              2053 GCAGAT-----GTATCAAATTCAATTTTAATCATTGATAAAATTGAATTTATACCAATT
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                           414 SerAsnSerGlnLysPheLysHisAsnLeuSerHisPheProLeuIleIleHisLysLeu
                                                1588 AAAATTGGATTAGCGCTAAATATATATATACAGGTGCATTAGGATGGACACACAGTAGT
                                                                                                                   AACAGTCTTGATACAAACTCTAAGGTAATTTGAAGGACCTGGTCATACAGGAGGAAACTTG
                                                                                                                                                   GTTTATTTTACAAAGTCAAGGGCGTTTAGAGATTACATGTAGAACTCCTAATTCTACAAA
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A library was constructed from Bacillus thuringlensis PS71M3 total cellular DNA in lambda Gem-11. Plasmid pMYC1636, selected in Escherichia coli, contained a 15 kb insert expressing a beta-endotoxin gene. This was sequenced (AAQ81180). A cured, acrystalliferous B.t. host carrying pMYC1636 produced a 77 kba crystal protein (AAR63079). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 TACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGTGATAATTTCGAGACA 192
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AsnlysAsnGluTyrGluIlePheAsnAlaProSerAsnGlyPheSerLysSerAsnAsn
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                                                                                                                                                                                                                                                                                              Method for controlling Calliphoridae pests - specifically utilises Bacillus thuringiensis isolates or toxins.
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94WO-US007902
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1318 TCAATTGTAACTGATAGACAAGTAACTCCCTACTTCCCCTTTTCCTAACATATACTTTACA 1377
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360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetala-------
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                                                                                                                                                         The sequence was deduced from the DNA sequence obtd. from plasmid pMYC1636 which was isolated from a genomic library prepd. from DNA from Et. PS71M3 [from B.t. PS71M3-69 (NRRL =18515)]. It is related to the crylVC toxins from B.t. var. israelensis. The protein has a mol. wt. of 77 kD. Microorganisms transformed with the DNA may be administered to dipteran insects or their environ. mente, the expressed toxins acting as an insecticide. See also ARA14373. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct PA
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                                                                                      Bacillus thuringiensis genes encoding diptera-active toxins - and transformed microbes used to control insects in various environments.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                   ThrTyrAlaAspPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu
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                                                                                                       GAAGGACCTGGTCATACAGGAGGAAACTTGGTTTATTTACAAAGTCAAGGGCGTTTAGAG
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567 ThrAsnAla-------ProLysThrThrValPheLeuThrGlyIleAspThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            delta-endotoxin; delta-endotoxin associate polypeptide;
expression cassette; transformation; transgenic; plant; bacteria;
lepidoptera; coleoptera; pest; pesticide; resistance;
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This sequence represents a delta-endotoxin crystal protein. This protein was included in the scope of the invention as a comparison to the delta-endotoxins of the invention. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have
                                                                                                                                                                                                                                                                                                                                     isolated delta-endotoxin and delta-endotoxin-associated nucleic acids polypeptides, useful for killing lepidopteran or coleopteran pests or producing organisms with pesticide resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGTGATAATTTCGAGACA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 ATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAAACCATTACAAAACACAAAT 132
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Matches:
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                                                                                                                                                                                                                     Koziel MG,
19-FEB-2004; 2004US-00782096.
19-FEB-2004; 2004US-00782141.
19-FEB-2004; 2004US-00783570.
19-FEB-2004; 2004US-00783417.
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È	430	AGCATAAAACAGCTAAAGTTACAAACTTTAGAAGGATTTAGACAAATATTACAA 483	<u>n</u>
qq	131	:::    :::      :::    AspLysAsnllelleAsnValLeuThrSerlleValThrProlleLysAsnGlnLeuAsp 150	0
à	484	AGCTATAATACAGCATTAGATGATTGGAGAAATTAAAAGACTACAAGCTCCTGGATTA 543	13
ąg	151	LysTyrGlnGluPhePheAspLysTrpGluProAlaArg163	£3
ò	544	CCACCATCATCAGCATTACAACAAGCTGCTTGACTCTTAAAATACGATTTGAGAATGTT 603	ε.
a a	164	ThrHisAlaAsnAlaLysAlaValHisAspLeuPheThrThrLeuGluProile 181	<b>T</b>
č	604	CACAATGATITIATICGAGAAATACCIGGITICCAACTIGAAACTIAIAAA 654	4.
Db Db	182	IleAspLysAspLeuAspMetLeuLysAsnAsnAlaSerTyrArgIleProThr 199	6
ć	655	ACGCTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAAATTTATTACAACAA 714	4
qq	200	LeuProAlaTyrAlaGlnIleAlaThrTrpHisLeuAsnLeuLysHis 216	91
č	715	GGIGCTGAATTGGCTGATGAATGGAATGCAGATATACATCCTTCACAAATTGAACCTAAT 774	4
DP DP	217	AlaalaThrTyrTyrAsnIleTrpLeuGlnAsnGlnGlylleAsnProSer 233	E.
ò	775	GCTGGAACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATATAGT 831	31
qq	234	ThrPheAsnSerSerAsnTyrTyrdlnGlyTyrLeuLysArgLysIleGlnGluTyrThr 253	53
ò	832	AACTATTGTGCAAATACCTATAGAGAAGAACTAAATAAACTTCGAAACGAACCTAATATG 891	1
g G	254	AspTyrCysileGlnThrTyrAsnAladiyLeuThrMetileArgThrAsnThrAsnAla 273	73
ò	892	AGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACTATC 951	11
Ωp	274	ThrTrpAsnMetTyrAsnThrTyrArgLeuGluMetThrLeuThrValLeuAspLeuile 293	93
ò	952	GCICAAITITICITITITAIGAIAIAAAAGAGATACAAAGAITICAAIAGGAAGAATAGGIGGC 1011	111
qq	294	AlallePheProAsnTyrAspProGluLysTyrProIleGly 307	70
È	1012	ATTABABCTGBACTTACABGBABATTTATACABCTGBABATBABITTTGACCGTCTTACT 1071	171
d d	308	vallysSerGluLeulleArgGluValTyrThrAsnValAsnSerAspThrPheArg 326	56
È	1072	TACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAATTTAACACGTTCAGGGCTT 1131	131
DP QD	327	ThrileThrGluLeuGluAsnGlyLeuThrArgAsnPro 339	39
È	1132	AGATTATTTTCATTTTTAGATGAACTTATATTTTTATACAAAAAAT 1170	176
Ob	340	ThrLeuPheThrTrp1leAsnGlnGlyArgPheTyrThrArgAsnSerArgAsp1leLeu 359	29
È	1177	GAAACCIAC	218
qq	360	AspproTyrAspilePheSerPheThrGlyAsnGlnMetAla373	73
à	1219		272
ą a	374	PheThrHisThrAsnAspArgAsnIleIleTrpGlyAlaValHisGlyAsnIle 392	92
è	1273	CCACCCACAACAAAAACTTTAATACCATTTGAATCCTATAAAGTT 131	1317
qq	393	IleSerGlnAspThrSerLysValPheProPheTyrArgAsnLysProlleAspLysVal 412	12
ć	1318	ICAAITICTAACTGATAGACAAGTAACTCCTACTTCCCTTTTCCTAACATATACTTTACA 137'	377
qq	413	GluileValargH18ArgGluTyrSerAsp 422	22
ò	1378	ATTAATCAAATTGAACTTTAATTTAAATACACCTAGTAATAAATTAACATATTCAGCT	1437
Dp	423	IlelleTvrGluMetIlePheSerAsnSerSerGluValPheArgTyrSerSer 441	41

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1915 ATACCACCTCAACGACTCAACAACACTTTTTCTCGGTACAATTATAAT-----AATTTA 1968
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                                    1798 ATTACATGTAGA---ACTCCTAATTCTACAATCTTATTACATTAGACTTCGATACGCT
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'Sequence 2, Application US/10782570
'Bublication No. US20040210965A1
'GENERAL INFORMATION:
'APPLICANT: Carozai, Nadine
'APPLICANT: Carozai, Michael G.
'APPLICANT: Cari, Michael G.
'APPLICANT: Cari, Brian
'TITLE OF INVENTION: Methods B.
'TITLE OF INVENTION: Methods for Its Use
'PRIOR REPRINCE: 2004-02-19
'PRIOR PRILING DATE: 2004-02-19
'PRIOR APPLICATION NUMBER: 60/448,812
'PRIOR PILING DATE: 2003-02-20
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Mismatches:
Indels:
US-10-782-570-1 (1-2235) x US-10-782-570-2 (1-744)
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Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 744
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-MODEL=Frame+ n2p.model -DBV=xlp
-Q=/cgn2 1/USFTO_spool p/US10782570/runat 12012006_060223_7574/app_query.fasta_1.2375
-Q=/cgn2 1/USFTO_spool p/US10782570/runat 12012006_060223_7574/app_query.fasta_1.2375
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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORS=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFFWT=pct -NORM=ext -HEARSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USGR=US10785570 @CGN 1 1 248 @runat 12012006_060223_7574
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-LONGLOG -DEV TIREOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPDP=10 -XGAPDF=10 -XGAPDF=10
                                                                                  January 12, 2006, 06:16:09; Search time 147 Seconds (without alignments) 12705.422 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
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               GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                            - protein search, using frame_plus_n2p model
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US-10-782-096-14
US-10-782-50-10
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AGICTIGATACAAACTCTAAGGTAATIGAAGGACCTGGTCATACAGGAGGAAACTIGGTT 1770
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                                                    1051 ATAAATTTTGACCGTCTTACTTACCTTGAAATTCAACCCAATCTCGCTATAATGGAATAT
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                                                US-10-104-30-4
Sequence 4, Application US/10782570
Sequence 4, Application US/10782570
Publication No. US20040210965A1
GENERAL INFORMATION:
APPLICANT: Carcil, Nadine
APPLICANT: Hardiss, Tracy
APPLICANT: Carcil, Michael G.
APPLICANT: Carcil, Michael B.
TITLE OF INVENTION: Methods for Its Use
TITLE OF INVENTION: Methods for Its Use
FILE REFERENCE: 045600/274144
CURRENT FILING DATE: 2004-02-19
PRIOR PPLICATION NUMBER: US/10/782,570
CURRENT FILING DATE: 2004-02-19
PRIOR PPLICATION NUMBER: 60/448,812
PRIOR PLICATION NUMBER: 60/448,812
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 694
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                 TYPE: PRT ORGANISM: Bacillus thuringiensis
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100.00%
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           2232
         221 TATGATATTGAT 223;
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                   21 PheProAsnArgAsnSerAsnAspSerArgTyrProTyrThrAsnAsnProAsnGlnPro
                                                                          TTACAAAACACAAATTACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGT
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**Boquence 2, Application US/10783417

**Publication No. US20040216186A1

**GENERAL INFORMATION:

**APPLICANT: Hargiss, Tracy

**APPLICANT: Hargiss, Tracy

**APPLICANT: Aciel, Michael G.

**APPLICANT: Carr, Micholas B.

**APPLICANT: Carr, Brian

**ITLE OF INVENTION: AXM-006, A Delta-Endotoxin Gene and

**ITLE OF INVENTION: AX
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CRCANISM: Bacillus thuringiensis
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                           CGTTTAGTTGGTATTGCGAATCGTAATAGATCTTATTGCTACGACAGGAACTGAAATT 1251
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RESULT 4 US-10-782-141-12

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112 AsnThr---TrpSerAspPhelleThrGlnThrLysAsnIlelleLysLysGlulleAla 130
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Publication No. US20040197917A1
GENERAL INFORMATION:
APPLICANT: Carcai, Nadine
APPLICANT: Carcai, Nachael G.
APPLICANT: Koziel, Micholas B.
APPLICANT: Koziel, Micholas B.
APPLICANT: Carr, Brian
TITLE OP INVENTION: AXMI-014, A Delta-Endotoxin Gene and
FILE REPERENCE: 04560/274143
CURRENT APPLICATION NUMBER: US/10/782,141
CURRENT APPLICATION NUMBER: 60/448,632
PRIOR FILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 1180
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Conservative:
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Percent Similarity:
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DB:
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US-10-782-141-12
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	Alignment Scores: 7.86e-87 Length: 1180  Pred. No.: 7.86e-87 Length: 2180  Score: 1180.00 Matches: 283  Percent Similarity: 54.55 Conservative: 131  Best Local Similarity: 37.29 Mismatches: 281  Query Match: 29.40 Mismatches: 64  DB: 4 Gaps: 25  US-10-782-570-1 (1-2235) x US-10-782-096-14 (1-1180)	
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13 AATAATAATGAATATGAGATTATCGATTCAAAGAATTTATCTTATC	GGACATTIGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATTGTATCGGT 	CTGTCTTT         rovalLeu GAGAAATT ::: hrLysAsn	427 GAAAGCATAAAACAGCTAAAGCTTACAAACTTTAGAAGGATTTAGAAATATTACAAAGC 486 :::       :::       131 SerThrTyrIleSerAsnalaAsnLysIleLeuAsnArgSerPheAsnValIleSerThr 150 487 TATAATACAGCATTAGATGATTAGAGAAAATTAAAAAGACTACAAGCTCCTGGATTACCA 546	547 CCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAGAATGTTCAC 606 11:	661 TTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAATTTATTACAACAAGGTGCT 720 :::	941 GCAAATACCTATAGAGACTAAATAAACTTCGAAACGAACCT
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CACAGTAGTGTTAATAGAAATAATGCAATATCAGATAAAATAATAATACATGATGCCCAGCA 1698 ATCAAAGGTAACAGTCTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGA 1758 1759 GGAAACTYGGTTTATTACAAAGTCAAGGGCGTTTAGAGATTACATGTAGAACTCCTAAT 1818 1879 CCTAATAȚATCTCTȚACAAȚACCAGGAGTAATAGGAATACCACCTCAACGACTCAACAAC 1938 CCAAGTACAGTAACATTACCTTTAAATCGAAACATACCATTTATATTTAATCGTGCAGAT 2058 1122 1233 1414 -----AGTAATAAATTAACATATTCAGCTGGGGAATTTATCTAATGATAAAAA 1464 1465 ACAACTGATTTTCCAATTTCCTGTAAAAAAGACTGTAAACCAATTATTAATCCAAATTGT 1524 ---ICCTATAAAATTGGATTAGCGCTAAATATATATATATACAGGTGCATTAGGATGGACA 1638 1123 TCAGGGCTTAGATTATTTTCATTTTTAGATGAACTTATATTTTATACAAAAAATGAAACG 1182 1294 ATACCATTIGAAICCIAIAAAGITICAAITGIAACIGAIAGACAAGIAACICCIACIICC 1353 413 471 LysasnilepheGlyLeuProileLeuLysargargGluasnGlnGlyasnProThrLeu 490 543 ::: ||| ||| ||| 432 LysTyrLeuAsnAsnIyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr 451 :::|||||| ::: ||| || 452 ArgLeuLeuGluLysGluLeuThr---AlaGlySerGlyGlnlleThrTyrAspValAsn 470 |||:::||||:: |dlyaspLeuile-----AspPheLysaspHisPheLysIleThrCysGlnHisSerAsn 581 ::: 394 IleSerGlnLy8SerSerValPheGlyAsnHisAsnValThrAspLysLeuLy8SerLeu 1063 CGTCTTACTTACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAATTTAACACGT 1183 TACGGGAATCGTTTAGTTGGTATTGCGAATCGTAATAGATCTTATGCT-----1234 ACGACAGGAACTGAAATTATATATGGAGAAAGAACAGGTCCACCACCACAAAAACTTTA 1582 1699 641 2059 1639 524 414

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1123 TCAGGGCTTAGATTATTTTCATTTTTAGATGAACTTATATTTTTATACAAAAAATGAAAACG 1182
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375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn 393
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                                                                                                                       TATAATACAGCATTAGATGATTGGAGAAAATTAAAAAGACTACAAGCTCCTGGATTACCA
                                                           151 TyrHisAsnHisLeuLysThrTrpGlu------AsnAsnProAsnProGln
                                                                                                                                                                           607 AATGATTTTATTCGAGAAATACCT-----GGTTTCCAACTTGAAACTTATAAAACGCTA
                                                                                                                                                                                                                                                        661 TTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATTACAACAAGGTGCT
                                                                                                                                                                                                                                                                                                                                  GAATTGGCTGATGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCTGGA
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                                                                                                   CCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAGAATGTTCAC
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AGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCCAAATCAACCATTACAAAAC 126
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|BanlysAsnGluTyrGluThrLeuAsnAlaSerGlnLysLysLeuAsnIleSerAsnAsn 25
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                                                       TTCACAAATCATACAAAAAATACTTTAAATATAGAAGCCACAAAACTATGATATTGAT 2232
                                                                           ThrvalleuThrGlyPheGlyPheThrThr-------proLeuGlyLeu----
                                                                                                                                                               Sequence 10, Application US/10782570

Sequence 10, Application US/10782570

Publication No. US20040210965A1

GENERAL INFORMATION:

APPLICANT: Carozal, Nadine

APPLICANT: Roziel, Michael G.

APPLICANT: Carr, Brian

TITLE OF INVENTION: AANI-007, A Delta-Endotoxin Gene and

TITLE OF INVENTION: Methods for Its Use

FILE REFERENCE: 045600/274144

CURRENT APPLICATION UNMBER: 00/448,812

PRIOR APPLICATION UNMBER: 2004-02-19

PRIOR PILING DATE: 2003-02-20

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PRESENCE: Mindows Version 4.0

SEQ ID NO 10

LENGTH: 1180

TYPE: PRI

CURRENT PRI

SOFTWARE: PRESENCE: CARO ANIONES CARO ANIONE
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Matches:
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Pred. No.:
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US-10-782-570-10
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|HisSerSerValAspProLysAsnThrIleTyrThrHisLeuThrThrGlnIleProAla
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                                               CACAGTAGTGTTAATAGAAATAATGCAATATCAGATAAAATAATTACAATGATCCCAGCA
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|TyAspLeuIle-----AapPheLysAspHisPheLysIleThrCysGlnHisSerAsn
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; Bequence 8, Application US/2040216186A1
; Bublication No. US20040216186A1
; GENERAL INFORMATION:
    APPLICANT: Carczzi, Nadine
; APPLICANT: Hargiss, Tracy
APPLICANT: Micholas B.
    APPLICANT: Carr, Brian
TITLE OF INVENTION: ARMI-006, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for Its Use
FILE REFERENCE: 045600/274146
CURRENT FILING DATE: 2004-02-20
FRIOR APPLICATION NUMBER: US/10/783,417
CURRENT FILING DATE: 2004-02-20
FRIOR PAPLICATION NUMBER: 60/448,806
FRIOR PAPLICATION NUMBER: 60/448,806
; NUMBER OF SEQ ID NOS: 15
; SOFTHARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 8
LENGTH: 1180
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; ORGANISM: Bacillus thuringlensis
US-10-783-417-8
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112 AsnThr---TrpSerAspPhelleThrGlnThrLysAsnIleIleLysLysGluIleAla 130
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166 AsnThrGlnAspValArgThrGlnIleGlnLeuValHisTyrHisPheGlnAsnValIle 185
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    Length:
Matches:
Conservative:
Mismatches:
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Query Match:
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	RESULT 8 US-10-781-979-14 Sequence 14, Application US/10781979 Fublication No. US20040250311A1 GENERAL INFORMATION: APPLICANT: Carozzi, Nadine APPLICANT: Hargyse, Trargy APPLICANT: Roziel, Michael G. APPLICANT: Carr, Brian TITLE OF INVENTION: Methods for Its Use TITLE OF INVENTION: Methods for Its Use TITLE OF INVENTION: Methods for Its Use TILE REFERENCE: 045600/274147 CURRENT PAPLICATION NUMBER: US/10/781,979 CURRENT PAPLICATION NUMBER: 60/448,797 PRIOR APPLICATION NUMBER: 60/448,797 NUMBER OF SEQ ID NOS: 28 SOFTWARE: FastSEQ for Windows Version 4.0 IENGTH: 1180 TYPE: PRT CORGANISM: Bacillus thuringiensis	Alignment Scores:     Score:     Score:
943 GATACTATCGCTCAATTTTCTTTTTTGATATAAGGATACAAAGATTCAATAGGAAGA 1002	ArgproHibleupherThrTrpLeuAspSerLeuAspPheTyrGluLysAlaGlnThr TACGGGAATCGTTAGTATTGCGAATCGTAATAGATCTTATGCT ThrProAsnAsnPhePheThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn ACGACAGGAACTGAAATATATATATATATATATATATATA	1525   TTACCAAGCTATAATAGTTATATATATATATATTATATT
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|SerProLysGlnLeuLeuGlnSer 41
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394 IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu
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Squerce 4, Application US/09756526A

Patent No. US20020038005A1

GENERAL INFORMATION:
GENERAL WOOLG-CHOWSKA
APPLICANT:
EVGENT, Mewina
APPLICANT:
GAILUAN:
GAILUAN:
GAILUAN:
FILE REFERENCE: 6-30913A
TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFORE TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFORE TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFORE TITLE OF INVENTION NUMBER: US/09/756,526A
CURRENT FILING DATE: 2001-01-08
PRIOR FILING DATE: 2000-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                       1879 CCTAATATATCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAACAAC 1938
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GlyAspLeulle-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn
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-- AGTAATAAATTAACATATTCAGCTGGGGGGAATTTATCTAATGATAAAAA
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300 IleGluLeuTyrThrGluSerValAlaGluGlyABpTyrLeuSerGlyIle------
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|TrpSerGlnPheMetLysHisGlyGluAspLeuLeuAsnGlnThrIleSerThrAlaVal 100
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AlabheAsnAspTrpLysArg------Ana----AsnProSerAla 131
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|SerSerAgpThrValAlaValValSerAlaGlyIleValValValGlyThrIleLeuThr
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; ORGANISM: Bacillus thuringiensis
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                   GCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAGAATGTTCACAATGATTTT
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Sequence 1. Application US/10345020

Publication No. US2030150018A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jana, Wojciechowska
APPLICANT: Eventin
APPLICANT: Ludmila, Revina
APPLICANT: Galunin
APPLICANT: Galunin
APPLICANT: Galunin
APPLICANT: APPLICANT: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
FILE REFRENCE: S-30913B
CURRENT PAPLICATION NUMBER: US 60/175,158
PRIOR APPLICATION NUMBER: US 60/175,158
PRIOR PLILNG DATE: 2000-01-07
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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TrpSerGlnPheMetLysHisGlyGluAspLeuLeuAsnGlnThrIleSerThrAlaVal 100
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US-10-345-020-4
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Percent Similarity:
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Query Match:
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1588 ANATTGGATTAGGCTAAATTATTATATAGGTGCATTAGGATGACACACAC	FILE REPRENCES: S. 3-90134C. FILE REPRENCES: S. 3-90134C. CURRENT APPLICATION NUMBER: US/10/342,821 FURNE PELIOR DATE: 2003-01-15 FRIOR PELIOR DATE: 2000-01-07 NUMBER OF SEQ ID NOS: S SOTWARE: Patentin version 3.0 SEQ ID NO 4 LENGTH: 1109 TYPE: PRT ORGANISM: Bacillus thuringiensis US-10-342-821-4 Alignment Scores:

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73 ATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACCATTACAAACACAAAT 132
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Conservative:
Mismatches:
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                                                                                                                         Sequence 17, Application US/10782141

Publication No. US20040197917A1

GENERAL INFORMATION:

APPLICANT: Carcazi, Nadine
APPLICANT: Roziel, Michael G.
APPLICANT: Carr, Brian

APPLICANT: Carr, Micholas B.
APPLICANT: Carr, Brian

TITLE OF INVENTION: AXMI-014, A Delta-Endotox

TITLE OF INVENTION: Methods for Its Use
FILE REFERENCE: 045600/274143

CURRENT APPLICATION WUMBER: US/10/782,141

CURRENT APPLICATION NUMBER: 60/48,632

FRIOR PILING DATE: 2003-02-20

NUMBER OF SEQ ID NOS: 23

SEQ ID NO 17

SEQ ID NO 17
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TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-782-141-17
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Query Match:
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 CTTATATTTTATACAAAAATGAAACGTACGGGAATCGTTTAGTTGGTATTGCGAATCGT 1215
                                                                                                                GAAAGAACAGGTCCACCCACAAAAA--------ACTTTAATACCATTT 1302
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| Asn------ThrAsnArgLeuSerLysGlnLeulleThrLeuLeuProGly 350
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484 AGCTATAATACAGCATTAGATGATTGGAGAAAATTAAAAAGACTACAAGCTCCTGGATTA 543 	544 CCACCATCATCACATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAGAATGTT 603 :::         :::         :::           :::	4	ACGCTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATTAAACAA 71.		AAACTTTTAAAAGAAAATATACCTAAATATAGT :::                   :::		892 AGATGGAGTATATTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACTATC 951	א-ט	1012 ATTAAAACTGAACTTACAAGAGAAATTTATACAACTGAAATAAAT	1072 TACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATTAACACGTTCAGGGCTT 1131	- 11 u 35		AAGAACAGGTi     aValHisGlyAsnIle	1273CCACCCACAAAAACTTTAATACCATTTGAATCCTATAAAGTT 1317	TCAATTGTAACTGATAGACAAGTAACTCCTACTTCCCCTTTTCCTAACATATACTTTACA 13	ATTAATCAAATTGAACTTTATTTAAATAATTCACCTAGTAATAAATTAACATATTCAGCT	GGGGGGATTTATCTAATGATAAAAAGAACTGATTTTCAATTTCCTGTAAAAAAGAC 	
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254 ABDTYrCygIleGlnThrTyrAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAa 273
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115 ValTrpGlnAspLeuLeuAsnIleGly------GlyArgProlleGlnGlulle
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1557 1177 GAAACGTAC------GGGAATCGTTTAGTTGGTATTGCGAATCGTAAT 1218 ---CCACCCACAAAAAACTITAATACCATTTGAATCCTAT------AAAGTT 1317 TCAATTGTAACTGATAGACAAGTAACTCCCTACTTCCCTAACTATACTTTACA 1377 1378 ATTAATCAAATTGAACTTTAATTAATTAATTCACCTAGTAATAAATTAACATATTCAGCT 1437 1558 ICCCAGTITICTITATITAATITATICCTATAAAATIGGATTAGCGCTAAATATATATAT 1617 1072 TACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATTAAATTTAACACGTTCAGGGCTT 1131 |||| ::: ::: SerTyrIleLysThrAspAsnTyrIlePheSerVal------ValArgGluArgArg 488 951 307 ||||::: ---PheThrHisThrAsnAspAspArgAsnIleIleTrpGlyAlaValHisGlyAsnIle 392 GAAGGACCTGGTCATACAGGAQGAAACTTGGTTTATTTACAAAGTCAAGGGCGTTTAGAG 1798 ATTACATGTAGA---ACTCCTAATTCTACACAATCTTATTACATTAGACTTCGATACGCT ||||||| Thrasnala------ProlysThrThrValPheLeuThrGly11eAspThr 1678 ATAATTACAATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAAACTCTAAGGTAATT ACAAATGGTGCTGGAAATACTCTTCCTAATATATCTCTTACAATACCAGGAGTAATAGGA :::|||:::|||||| ||||||::||| ||| :::||| ||| 308 ValLysSerGluLeulleArgGluValTyr---ThrAsnValAsnSerAspThrPheArg ||||||| 413 GluIleValArgHisArgGlu-----TyrSerAsp |||| |IelleTyrGluMet1lePhePheSerAsnSer---SerGluValPheArgTyrSerSer ::: ||||::: ||||::: ||| |||||| |||||| sanSerThrIleProLysGlnThr 1498 IGTAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTATAGTCATATTTA 462 Trplys------AsnGluGluTyrGlyHisThrLeu GCTCAATTTTTTTTTTTTTATAAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGC 392 AGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACTATC 1132 AGATTATTTTTTTAGATGAACTTATATTTTTATACAAAAAT-----1318 423 1738 1855 267 1273 472 509 529 952 327 374

64 PheAlaSerSerGluThrIleValGlyValSerAlaGlyIleIleValValGlyThrWet 83 253 TAGCCOGTARGCTCACTCTATATCCGACCGATGGAATAATGGTGCTATA 312	274 952 294 1012 308 1072 327 1132 340 1177 360 1219
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567 ThrAgnala------ProLysThrThrValPheLeuThrGly1leAspThr 581
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                                                                 413 GluilevalargHisArgGlu-----------TyrSerAsp 422
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115 ValTrpGlnAspLeuLeuAsnIleGly------GlyArgProIleGlnGluIle 130
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APPLICANT: Carozzi, Nadine
APPLICANT: Carozzi, Nadine
APPLICANT: Koziel, Michael G.
APPLICANT: Koziel, Michael G.
APPLICANT: Carr, Brian
TITLE OF INVENTION: AXMI-006, A Delta-Endotoxin Gene and
TITLE OF INVENTION: AXMI-006, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for Its Use
FILE REPERENCE: 045600/274146
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: 60/448,806
PRIOR FILING DATE: 2003-02-20
SOFTWARE: PeatsEQ for Windows Version 4.0
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RESULT 15 US-10-783-417-12 Sequence 12, Application US/10783417 ; Publication No. US20040216186A1

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655	ACGCTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAATTTTACAACAA 714
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715	GGTGCTGAATTGGCTGATGAATGCAGATATACATCCTTCACAAATTGAACCTAAT 774 
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1012	ATTAAAACTGAACTTACAAGAGAATTTATACAACTGAAATAAAT
1072	TACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAAATTTAACACGTTCAGGGCTT 1131
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1273	CCACCCACAACAAAAACTTTAATACCATTTGAATCCTATAAAGTT ::
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1378	ATTAATCAAATTGAACTTTAAATAATTCACCTAGTAATAAATTAACATATTCACCT
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1969 CAATACGGAGATTTTGGGTATTTCCAATTTCCAAGTACAGTA------- 2010
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1678 ATAATTACAATCACAGCAATCAAAGGTAACAGTCTTGATACAAACTCTAAGGTAATT 1737
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567 ThrasnAla------ProLysThrThrValPheLeuThrGly1leAspThr 581
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i Sequence 4, Application US/11058727

j Publication No. US20050261483A1

j Publication No. US20050261483A1

j Publication No. US20050261483A1

j RUBICANT: Andre R. Abad

j APPLICANT: Rafael Herrmann

j APPLICANT: Theodore W. Kahn

j APPLICANT: Theodore W. Kahn

j APPLICANT: James K. Presnail

j APPLICANT: James K. Presnail

j APPLICANT: James F.H. Wong

j TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

j APPLICANT: James F.H. Wong

j TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

j APPLICANT: S18/287809

CURRENT APPLICATION NUMBER: US/11/058,727

CURRENT PILING DATE: 2002-06-26

j PRIOR FILING DATE: 2003-04-04

pRIOR PILING DATE:
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Sequence 6, Appli
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3: /cgn2 6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

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                          GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-11-192-801-4
US-11-058-727-2
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Pred. No.:         8.59e-48         Length:         1210           Score:         716.00         Matches:         216           Percent Similarity:         44.81\$         Conservative:         138           Best Local Similarity:         27.34\$         Mismatches:         304           Query Match:         18.18\$         Indels:         30           DB:         7         Gaps:         30	-782-570-1 (1-2235) x US-11-058-727-4 (1-1210)	1 GTGAATCAAAATAATAATGAATATGAGATTATCGATTCAAAGAATTTATCTTATCCT 60	MetSerProAsnAsnGlnAsnGluTyrGluIleIleAspAlaThrProSerThrSerVal	61 TCTACCAGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACCATTA 120 		:::      :::::                :::::	178 GATAATTTCGAGACATTTGCTAGTGCTGATTGCTGCAGTTAGTGCAGGTACTATT 237	58 GlySerProGluValLeuValSerGlyGlnAspAlaAlaLysAlaAlaIleAsp 75	GTATCCGGTACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGA	76 IleValG1yLysLeuLeuSerG1yLeuG1yValPro 8	298 ATAATAGSTGCTATAATAATATTSTTTGGTACCCTAATCACTGTCTTTTGGCCCGCGGGA 357   ::	GAACAAGACAAAACAGTATGGACACAATTTATTAAAATGGGAAAATTTTTGTTGATACA	08 GlnLysSerGlnTrpGluIlePheMetGluGlnValGluGluLeuIleAsnGln		:::     :::       :::     :::	478 TTACAAAGCTATAATACAGCATTAGATGATTGGAGAAAATTAAAAAGACTACAAGCTCCT 537	146 TyrGlnLeuTyrLeuThrAlaLeuGluGluTrpLygGlu158	GGATTACCACCATCATCAGCATTACAACAAGCTGCCTTGACTTTAAAATACGATTTGAG	159AenProAenGlySerArgAlaLeuArgAepValArgAenArgPheGlu 174	AATGITCACAATGATTITIATICGAGAAATACCTGGTTTCCAACTTGAAACTTATAAAACG			THE STATE OF THE S		GGGAACATCAGATGACTATTATAAAACTTTTTAAAAGAAAATATACCTAAATGTAAGTAA	:::::        :::: ThrThrIleAsnAsnTyrTyrAspArgGlnMetLysLeuThrAlaGluTyrSerAspHis	838 TGTGCAAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACCTAATATGAGATGG 897		898 AGTATATTAATGATTATGGAATATATGACTATTACTGTATTAGATACTATCGCTCAA 957	266 ValAspTyrAsndlnPheArgArgGluMetThrieuThrValLeuAspValValAlaLeu 285
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11	126 GGGCTTAGATTATTTTCATTTTTTAGAACTTATATTTTATACAAAAAATGAAAGG 1182 340 ProHisValPheAspTyrIleThrGlyLeuThrValTyrThrGlnSerArgSerIle 358
11	183TACGGAATCGTTTAGTTGGTATTGCGAATCGTAATAGATCTTAT 1230 
12	231 GCTACGACAGGAACTGAAATTATATATGGAGAAAGAACAGGTCCACCACAACAAAAACT 1290 :::
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17.	702 AAAGGTAACAGTCTT
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17	98 ATTACATGTAGAACTCCTAATTCTACACATCTTATACATTAGACTTCGATACGCTACA 1857 ::
18	SB AATGGTGCTGGAAATACTCTTACTATACAATACCGAGGTAATAGGAATA 1917 
19	118 CCACCTCAACGACTCAACAACACTTTTTCTGGTACAAATTATAATAATTACAATACGGA 1977

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TTTTCTTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGCATTAAA 1017
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JAPPLICANT: ADDAG
APPLICANT: Ronald D. Flannagan
APPLICANT: Ronald D. Flannagan
APPLICANT: Refael Hermann
APPLICANT: Theodore W. Kahn
APPLICANT: Bliry Fred McCutchen
APPLICANT: James K. Presnail
APPLICANT: James K. Presnail
APPLICANT: James K. Wong
APPLICANT: Geo-Guo Yu
ITILE OF INVENTION: Genes Encoding Proteins With Pesticidal
ITILE OF INVENTION: Genes Encoding
FILE REFERENCE: 35718/291049
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR PRILING DATE: 2003-04-04
PRIOR PILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
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PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20050261188A1
GENERAL INFORMATION:
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                                                      // Sequence 4, Application US/11192801
/ Publication No. US20050273882A1
/ GENERAL INFORMATION:
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                                                                                                                   ||| :::||| :::||| ::- PheAspPheThrAsnIyrAspIleTyrLysThrLeuSerLysAspAlaValLeuLeu 417
                                                                                                                                                                                                                                                                                                                                                                                   510 ArgSerAlaAspLeuIleAsnAlaValHisSerAspLysIleThrGlnIleProValVal 529
                                                                                                                                                                                                                                  MetValAsn-----GlnLeuAsnAsnThr 445
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                     SerSerAlaArgTyrIleArgHisTrpAlaGlyHisGlnIleSerTyrHisArgIlePhe
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ThrArgAmpSerGluLeuGluLeuProProGluThrSerAmpGlnProAmTyrGluSer
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LysValSerAspLeuAlaProSerIleThrGlyGlyProAsnAsnThrValValSerGly
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                                                                                                                                                       ACTTCCCCTTTTCCTAAC-----ATATACTTTACAATTAATCAAATTGAACTTTAT
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---SerlleProAlaThrGlySerThrThrGlyLeuValProValPheSerTrpThrHis
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APPLICANT: Romano, Charles P.

TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants FILE REFERENCE: 38-21(15)304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/11/192,801
CURRENT FILING DATE: 2005-07-29
PRIOR APPLICATION NUMBER: US/10/232,665
PRIOR APPLICATION NUMBER: US/10/232,665
PRIOR APPLICATION NUMBER: US/10/232,665
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 4
LENGTH: 652
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Matches:
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Mismatches:
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Gaps:
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2086 AAAATTGAATTTATACCAATT 2106
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|HisLeuPheAspTyrLeuGlnGlyIleGluPheHisThrArgLeuGlnProGlyTyrSer 352
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                                AACTATTGTGCAAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACCTAATATG 891
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                    GCTCCTGGATTACCACCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAAATACGA 591
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541 LeuPheLeuLysGluSerSerAsnSerIleAlaLysPheLysValThrLeuAsnSerAla 560 1990 TICCAATITCCAAGTACAGTACATTACCTTTAAATCGAAACATACCATTT-----1648 GTTAATAGAAATAATGCAATATCAGATAAAATAATTACAATGATCCCAGCAATCAAAGGT 1708 AACAGTCTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAGAAACTTG GTTTATTTACAA-----AGTCAAGGCGTTTAGAGATTACATGTAGAACTCCT 587 AsnaspPhelleVallleTyrIleAsnLysThrMetAsnIleAspAspLeuThrTyr 1588 AAAATTGGATTAGCGCTAAATATATTATATACGGGGGCCATTAGGATGGACACACAGTAGT APPLICANT: Ronald D. Flannagan
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Theofore W. Kahn
APPLICANT: Theofore W. Kahn
APPLICANT: James F. H. Wong
APPLICANT: James R. Presnall
APPLICANT: Gao-Guo Yu
APPLICANT: Gao-Guo Yu
APPLICANT: Gao-Guo Yu
APPLICANT: Cao-Guo Yu
APPLICANTON: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Garlety
FILE REFERENCE: 35718/287809
CURRENT PILING DATE: 2005-02-15
FRIOR APPLICATION NUMBER: 60/460,787
FRIOR FILING DATE: 2003-04-04
FRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SCOFTWARE: FastSEQ for Windows Version 4.0

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                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                    US-10-782-570-1 (1-2235) x US-11-058-727-2 (1-1206)
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-058-727-2
                                             1.72e-46
699.00
45.26%
27.43%
                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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1459 AAAAAAACAACTGATTTTCAATTTCCTGTAAAAAAAAGACTGTAAAACCAATTATTAATCCA 1518 1018 ACTGAACTTACAAGAGAAATTTATACAACT-----GAAATAAATTTGACCGTCTT 1068 1126 GGGCTTAGATTATTTTCATTTTTAGATGAACTTATATTTTATACAAAAAATGAAACGTAC 1185 1186 GGGAAT---CGTTTAGTTGGTATTGCGAATCGTAATAGATCTACTTAT-----GCTACG 1236 1348 ACTTCCCCTTTTCCTAAC-----ATATACTTTACAATTAATCAAATTGAACTTTAT 1398 1399 TTAAATAATTCACCTAGTAATAAATTAACATATTCAGCTGGGGGAATTTATCTAATGAT 1458 1612 TTATATACAGGT---------GCATTAGGATGGACACACAGTGTGTT 1650 1651 AATAGAAATAATGCAATATCAGATAAAATAATTACAATGATCCCAGCAATCAAAGGTAAC 1710 AGTCTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAGAAACTTGGTT 1770 1291 TTAATACCAȚȚTGAATCCȚAȚAAAGTT---TCAATTGTAACTGATAGACAAGȚAACTCCT 1347 1552 ATTTTATCCCAGTTTTCTTTATTTATTTCCTATAAATTGGATTAGCGCTAAATATA 1611 TTAGAGATTACATGTAGAACTCCTAATTCTACACAATCTTATTACATTAGACTTCGATAC 1851 246 CysValLysTrpTyrGluThrGlyLeuAlaLysLeuLysGlyThrSerAlaLysGlnTrp 265 ||| |||||| ::: ||| 286 PheProAenTyrAegThrTyrProMetGlu-------ThrLys 299 ::: ||| ::: ::: ||| 359 SerSerAlaArgTyrIleArgHi8TrpAlaGlyHi8GInIleSerTyrHi8ArgValSer 378 418 AspileValTyrProGlyTyrThrTyrIlePhePheGlyMetProGluValGluPhePhe 437 485 ArgleuCysHisIleThr----Serile 492 493 ProalarhrdlyAsnThrThrGlyLeuValProValPheSerTrpThrHisArgSerAla 512 ::: |||||| ||| ||| AspleudandanthriletyrSerAsplysllethrGlnileProAlaValLysCysTrp 532 533 AspAsnLeuProPheValProValValLysGlyProGlyHisThrGlyGlyAspLeuLeu 552 -----CGT 1791 ---ACTTACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAATTTAACACGTTCA GlySerTrpTyrAspLysAlaProSerPheGlyValIleGluSerSerValIleArgPro 340 Pro---HisValPheAspTyrIleThrGlyLeuThrValTyrThrGlnSerArgSerIle TITICITITIATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGCATTAAA 1237 ACAGGAACTGAAATT----ATATATGGAGAAAGAACAGGTCCACCACAAAAACT GlnTyrAsnArgSerThrGlySerValGlyThrLeuPheLeuAlaArgTyrGlyLeuAla ---TATTTACAAAGTCAAGGG-------

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                                                                                       1972 TACGGAGATTTTGGGTATTTCCAATTTCCAAGTACAGTAACATTACCTTTAAATCGAAAC 2031
GCTACAAATGGTGCTGGAAATACTCTTCCTAATATATCTCTTACAATACCAGGAGTAATA 1911
                                                                                                                                                                               600 IleGlnMetProLygThrMetAsnProGly-------GluAspLeuThr 613
                                                                                                     586 AlaThraspala---------AspilevalLeuHisvalAsnaspalaGln
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Publication No. US20050261188A1

GENERAL INFORMATION:

APPLICANT: Andre R. Abad

APPLICANT: Refael Herrmann

APPLICANT: Rafael Herrmann

APPLICANT: Albert L. Lu

APPLICANT: Billy Fred McCutchen

APPLICANT: James K. Presnail

APPLICANT: James K. Presnail

APPLICANT: James R. Wong

APPLICANT: Cac-Guo Yu

TITLE OF INVENTION: Activity

FILE REFRENCE: 35718/291049

CURRENT APPLICATION NUMBER: 60/460,787

PRIOR FILING DATE: 2002-06-26

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-06-25

NUMBER OF SEQ.ID NOS: 134

SOFTWARE: Faster For Windows Version 4.0

SEQ ID NO 2

SEQ ID NO 2
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Matches:
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|LeuArgProGlyValThrAgpTyrGluValAsn 700
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|Glu-----LysSerGlnTrpGluIlePheMetGluGlnValGluLeuIleAsnGln 125
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286 PheProAsnTyrAspThrArgThrTyrProMetGlu--------ThrLys 299
                                                                                                                            CAAAACACAAATTACAAAGAGTGGCTCAATATGTGTCAAGGGAAT---ACACAATATGGT 177
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GlyserProGluValLeuValSerGlyGlnAsp-----AlaAlaLysAlaAlaIleAsp
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                                                       TCTAACAGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACCATTA
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                                                                        1186 GGGAAT---CGTTTAGTTGGTATTGCGAATCGTAATAGATCTACTTAT-----GCTACG 1236
                                                                                                                      1237 ACAGGAACTGAAATT-----ATATATGGAGAAAGAACAGGTCCACCCACAAAAAAGT 1290
                                                                                                                                                                      TTAATACCATTIGAATCCTATAAAGTT---TCAATTGTAACTGATAGACAAGTAACTCCT 1347
                                                                                                                                                                                                                    1348 ACTICCCCTITICCIAAC-----AIAIACTITACAATTAATCAAATTGAACTITAT 1398
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                                       1552 ATTTTATCCCAGTTTTCTTTATTTAATTATTCCTATAAATTGGATTAGCGCTAAATATA 1611
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GlySerTrpTyrAspLysAlaProSerPheGlyValIleGluSerSerValIleArgPro 339
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600 IleGlnMetProLygThrMetAsnProGly--------GluAspLeuThr 613
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Sequence 6, Application US/11192801
; Sequence 6, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; FAPLICANT: Romano, Charles 8
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; TITLE OF INVENTION: Improved Exp. Corn
; CURRENT PELING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: synthetic or OTHER INFORMATION: non-naturally occurring amino acid sequence encoded by SEQ ID
2199
                                                                                                                                      671 AspLeuGluAlaAlaYsLysAlaValAsnAlaLeuPheThrAsn---ThrLysAspGly 689
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58 AgpAsn-----SerThrValLysAspAlaValGlyThrGlyIle 70
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|LeuArgProGlyValThrAspTyrGluValAsn 700
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                                                                            775 GCTGGAACATCAGATGACTATTATAAACTTTTAAAAGAAATATACCTAAATATAGTAAC 834
                                                                                                                                                                                                                                                                                                                                         224 GluaspvalalaGlupheTyrHisargGlnLeuLysLeuThr---GlnGlnTyrThrasp 242
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243 HisCysvalAsnTrpTyrAsnValGlyLeuAsnGlyLeuArgGlySerThrTyrAspAla 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 LeuPheProPheTyrAspileArgLeuTyrSerLys-------GlyVal 296
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334 LeuPheAspTyrLeuGlnGlyIleGluPheHi8ThrArgLeuGlnProGlyTyrPheGly 353
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                                                               415 ACACCGTTAACAGAAAGCATAAAACAGCTAAAGTTACAAACTTTAGAAGGATTTAGACAA 474
                                                                                                                                                                       154 -----ThrProLeuSerLeuArgSerLysArgSerGlnAspArgIleArgGluLeuPhe 171
                                                                                                                                                                                              GAGAATGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAA 654
                                                                                                                                                                                                           655 ACGCTATTACCTACTTATGCGCAAGCTGCTAATTTTCATTTAAATTTTACAACAA 714
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                                    GGAGAACAAGACAAAACAGTATGGACACAATTTTATTAAAATGGGAGAAATTTTTGTTGAT
                                                                                                         ATATTACAAAGCTATAATACAGCATTAGATGATTGGAGAAAATTAAAAAGACTACAAGCT
                                                                                                                            140 AsnPheGluAspTyrValAsnAlaLeuAsnSerTrpLysLys------
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1780 AGTCAAGGGCGTTTAGAGATTACATGTAGAACTCCTAATTCTACACAATCTTATTACATT 1839
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---ACATATTCAGCT--- 1437
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                                                                                                                                                               493 PhePheThr------TrpThrHisArgSerValAspPhePheAsnThrIleAsp 508
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569 ArglleArgTyrAlaSerThr-------ThrAsnLeuArgLeuPheVal 582
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1390 GAACTTTATTTAAATAATTCACCTAGTAATAAATTA----
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RESULT 7
US-11-192-801-2
i Sequence 2, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:

APPLICANT: Romano, Charles P.

TILLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants FILLE REFERENCE: 38-21(15204) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/11/192,801
CURRENT FILING DATE: 2005-07-29
PRIOR APPLICATION NUMBER: US/10/232,665
PRIOR PILING DATE: 1090-08-29
PRIOR PILING DATE: 1999-08-19
NUMBER: 1999-08-19
NUMBER: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0

TYPE: PRT ORGANISM: Bacillus thuringiensis

US-11-192-801-2	1-801-2	ī	
Alignment Scores		<b>a</b>	263 TrpValLysPheAsn
Score: Percent Similari	6.41e-46 Length: 652 691.00 Matches: 208 Similarity: 44.84 Conservative: 122	ç d	955 CAATTITCITTITATO
Query Match DB:	ailly: 20.20* M.B.MacCheB: 17.54* Indels: 7 Gaps:	8	1015 AAAACTGAACTTACAA
US-10-782	3-570-1 (1-2235) x US-11-192-801-2 (1-652)	යු ,	297 LysThrGluLeuThr
È	BAATCAAAATAATAATGAATATGAGATTATCGATTCAA	දි සි	1075 CTTGAAATTCAACCC
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È	61 TCTAACAGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACCATTA 120	<b>3</b> 8	
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8	GGAATAATAGGTGCTATAATAATAATCHTTTGGTACCCTAATCACTGTTTTGGCCCGCG	È	1342ACTCCTACTT
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ે	GGAGAACAAGACAAGATATGGACACAATTTATTAAAATGGGGAAGAATTTTGTTGAT	È	1390 GAACTTTATTTAAAT
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ර ර	GAGAATGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAA	q Q	:::    493 PhePheThr
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අු	11. 1 AlaGlnValPheGlyGluGluTrpGlyTyrSer	qa (	529 IleileGluGlyProc
ò	775 GCTGGBACATCAGATGACTTTAAAACTTTTAAAAGAAAATATACCTAAATATAGGAAC 834	è 1	∢
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PACAAATGGTGCTGGAAATACTCTTCCTAATATATCTCTTACAATA 1899
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| :::||| ::::| | OthrPheLeuSerlleGluAsnSerlleArgLysPro-----His 333
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uGlnGlyIleGluPheHisThrArgLeuGlnProGlyTyrPheGly 353
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|TyrTrpSerGlyAanTyr-----ValGluThrArgProSer 370
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1279 ACA-----ACAAAAACTTTAATACCATTTGAATCCTATAAAGTTTCAATTGTAACT 1329
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162 IleThrArgLeuAspGlyLeuGlyAsnValLeuAlaLeuTyrGlnLysAlaPheGluGlu 181
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|------SerdlnThrHisValAsn-------AspAsnTyrAsnLeuGln 261
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ThrGlyGlnValArgSerGlyAsp------GlyAsnSerAsnTyrTyrTrpLysSer 389
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                                                                                                                                                                                                                                                                            Sequence 6, Application US/11091643
Sequence 6, Application US/11091643
Publication No. US20050246789A1
GENERAL INPORMATION:
APPLICANT: TANAKA, Masao
APPLICANT: TANAKA, Masao
APPLICANT: HASEGRAW, Maketo
APPLICANT: HASEGRAW, Maketo
APPLICANT: HASEGRAW, Maketo
APPLICANT: HASEGRAW, Masaharu
APPLICANT: KIMURA, Masaharu
APPLICANT: KIMURA, Masaharu
APPLICANT: KIMURA, Masaharu
APPLICANT: KIMURA, Masaharu
APPLICANT: NINTHIABAH, Hideli
TITLE OF INVENTION: POlypepide having larvae growth inhibiting or
TITLE OF INVENTION: Polypepide having the same
FILE REFERENCE: OP1335
CURRENT APPLICATION NUMBER: US/11/091,643
CURRENT FILING DATE: 2005-03-29
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR APPLICATION NUMBER: JP 2001-203463
PRIOR APPLICATION NUMBER: JP 2001-64-33
PRIOR APPLICATION NUMBER: JP 2001-203463
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683.50
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ORGANISM: Bacillus popilliae
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Best Local Similarity:
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Pred. No.:
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US-11-091-643-6
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US-11-091-643-6
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             ---GluAshGlnArgValPheProAla 470
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LysGlnGlnLeuGluLysAlaArgLysAlaValAsnHisLeuPheThrAspGlySerLys 704
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Sequence 8, Application US/11192801; Publication No. US20050273882A1; GENERAL INFORMATION:

RESULT 9 US-11-192-801-8

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by SEQ ID
         Plants
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TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in I
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/11/192,801
CURRENT FILING DATE: 2005-07-29
PRIOR PILING DATE: 2005-08-29
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATCHIN VET. 2.0
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                                                                                                                                                                                                                                                                                                                            sequence for Cry3Bb variant v11231 encoded
                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: non-naturally
OTHER INFORMATION: occurring amino acid sequence encoded by SEQ ID NO:7
FEATURE:
NAME/KEY: PRT
LOCATION: (1)..(653)
OTHER INFORMATION: amino acid sequence for Cry3Bb variant v11231 encoded
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Matches:
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Best Local Similarity:
Query Match:
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US-11-192-801-8
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AGTCATATTTATCCCAGTTTTCTTTATTTATTATTCCTATAAAATTGGATTAGCGCTA 1605
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                                                                                                                                                                                                                                                                                                                334 ---HisLeuPheAspTyrLeuGlnGlyIleGluPheHisThrArgLeuGlnProGlyTyr 352
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              ::: ||| ::: ::: ||| GlnalaGluSerHigPheArgAgnSerMysPheGluVal 193
                                                 CTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTTACAACAAGGT 717
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Sequence 10, Application US/11192801

Sequence 10, Application US/11192801

Sequence 10, Application No. US20050273882A1

Sequence 10, Application No. US20050273882A1

Sequence 10, Application No. US20050273882A1

TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants

PILE REFERENCE: 38-21(1534) Cry3Bb Improved Exp. Corn

CURRENT APPLICATION NUMBER: US/11/192,801

PRIOR PILING DATE: 2002-00-29

PRIOR FILING DATE: 1099-08-19

NUMBER OF SEQ ID NOS: 43

SOFTWARE Patentin Ver. 2.0

SEQ ID NO 10

IERNGTH: 653
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                                                                        1725 ATATCAGATAAATAATTACAATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAAAC 1725
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1606 AATATTATATACAGGTGCATTAGGATGGACACACAGTAGTGTTAATAGAAATAATGCA 1665
                                                                                                                                                                                                                           -----AGTCAAGGGCGTTTAGAGATTACATGTAGAACTCCTAATTCTACACAATCTTAT 1833
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                                                                                                                                                                                                                                                                                                                        594 TyrileAsnLysThrMetAsnLysAspAspAspLeuThrTyrGlnThrPheAspLeuAla 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: non-naturally OTHER INFORMATION: occurring amino acid sequence encoded by SEQ ID NO:9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 614 ThrThrAsnSerAsnMetGlyPheSerGlyAspLysAsnGluLeuIleileGlyAlaGlu
                       2053 GCAGATGTATCAAATTCAATTTTAATCATTGATAAAATTTGAATTTATACCAATT 2106
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qa		a	315 ThrieuGlniyaTyrGlyProj
Š	64 AACAGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACCATTACAA 123	È	1129 CTTAGATTATTTTCATTTTAC
	20 GluLeuGlnThrAsnHisAsnGlnTyrProLeuAlaAspAsnProAsnSerThrLeuGlu 39	a	HisLeupheAspT
9,	24 AACACAAATTACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGTGAT 180	à	1174AATC
<b>q</b> a	40 GluLeuAsnTyrLysGluPheLeuArgMetThrGluAspSerSerThrGluValLeuAsp 59	ପ୍ର	
9	181 AATTTCGAGACATTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATT 237	È	1216 AATAGATCTACTTATGCTACG
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	95 PheAlaGlvAlaLeuThrSerPheTvrGlnSerPheLeuAsnThr11eTrnProSer 103	q	404 ThrilealaAsnThrAspVal
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		ò	1606 AATATATATAÇAGGTGCA
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	174 GlnAlaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPheGluVal 193	ò	1666 ATATCAGATAAAATAATTACAA
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, ,	718 GCTGAATTGGCTGATGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCT 777 :::	2 8	528 AlaSerlleIleGluGlvProC
Dp	214 GlnValPheGlyGluĠluİrpGlyTyr	È	1780aGTCAAGGGGGTTTAG
7	778 GGAACATCAGATGACTATTATAAACTTTTAAAAGAAATATACCTAAATAT 828	; A	
	23SerSerGlukspValAlaGluPheTyrArgArgGlnLeuLysLeuThrGlnGlnTyr 241	ò	1834 TACATTAGACTTCGATACGCTA
	829 AGTAACTATTGTGCAAATACCTATAGAGGAGGACTAAAATAAACTTCGAAACGAACCTAAT 888 ::::::::	<b>a</b>	:::         :::   ::: 568 ArgValArgIleArgTyrAlaS
Dp	42 ThraspHisCysValAsnTrpTyrasnValGiyLewAsnGlyLeuArgGlySerThrTyr 261	Š	1894 ACAATACCAGGAGTAATAGGAA
	889 ATGAGATGGAGTATATTTAATGATTATGGAGATATATGACTATTACTGTATTAGATACT 948	<b>3</b> 8	:: 582 PheVal
	62 AspAlaTrpValLysPheAsnArgPheArgArgGluMetThrLeuThrValLeuAspLeu 281	ò	1954 AATTATAAT
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GAAACGTACGGGAATCGTTTAGTTGGTATTGCGAATCGT 1215 SACAGGAACTGAAATTATATATGGAGAAAAGAACAGGTCCA 1275 AATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTAT 1545 FTCTTTATTTAATTACCTATAAAATTGGATTAGCGCTA 1605 ATTAGGATGGACACACAGTAGTGTTAATAGAAATAATGCA 1665 ATTACCTTTAAATCGAAACATACCATTTATATTTAATCGT 2052 FTCCCCTTTTCCTAAC-----ATATACTTTACAATTAAT 1383 ITTATCTAATGATAAAAAAAAACAACTGATTTTCAATTTCCT 1485 AATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAAAC 1725 regreatacaggaaggaagcriggtttattitacaa---- 1779 AGAGATTACATGTAGAACTCCTAATTCTACACAATCTTAT 1833 AATACCACCTCAACGACTCAACACACTTTTTCTGGTACA 1953 PAATCTCGCTATAATGGAATATAATTTAACACGTTCAGGG 1128 ACCATTTGAATCCTATAAAGTTTCAATTGTAACTGATAGA 1335 PAATTCACCTAGTAATAATTA-----ACATATTCA 1434 PACAAATGGTGCTGGAAATACTCTTCCTAATATATCTCTT 1893 ------AATTTACAATAÇGGAGATTTTGGGTATTTC 1992 | ::: |||:::|||::: |GlnGlyIleGluPheHisThrArgLeuArgProGlyTyr 352 nTyrTrpSerGlyAsnTyr-----ValGluThrArg 369 SerPheAspGlyGlnLysValTyr-----Arg 403 ::: :::||||||| |AlaalaTrpProAsnGlyLysValTyrLeuGlyValThr 423 ValSerAlaGlnAspSerIleAsp-----GlnLeuPro 461 aGluCysPhereuMetGlnAspArgArgGlyThrIle--- 492 | :::||| :::||| cglnLeuProValValLysAlaTyrAlaLeuSerSerGly 527 ::::::||| eLygValThrLeuAgnSerAlaAlaLeuLeuGlnArgTyr 567 |::: |sSerThr-----ThrAgnLeuArgLeu 581 ------GinAsnSerAsnAsnAspPheLeuValile 593 :::||| nLysAspAspLeuThrTyrGlnThrPheAspLeuAla 613 :::::||| PheSerGlyAspLysAsnGluLeuIleIleGlyAlaGlu 633 AGATGAACTTATATTATACAAAA-------

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-------AATGAAACGTACGGAATCGTTTAGTTGGTATTGCGAATCGT 1215
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LyslleGluGluTyrAlaLysSerLysAlåLeuAlaGluLeuGlnGlyLeuGlnAsnAsn 141
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TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants FILE REPERRNCE: 38-21(15304) Cry3Bb Improved Exp. Corn CURRENT APPLICATION NUMBER: US/11/192,801

CURRENT APPLICATION NUMBER: US/11/22,665

PRIOR APPLICATION NUMBER: US/10/212,665

PRIOR APPLICATION NUMBER: US/09/377,466

PRIOR PILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 43

SOFTRARE: Patentin Ver. 2.0

SEQ ID NO 12

LENGTH: 653
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PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnThrIleTrpProSer--- 103
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OTHER INFORMATION: amino acid sequence encoded by SEQ ID NO:11
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; Sequence 12, Application US/11192801
; Publication No. US20050273882A1
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Sequence 14, Application US/11192801

Publication No. US20050273882A1

GENERAL INFORMATION:

APPLICATY: ROMANO, Charles P.

TITLE OF INVENTION: Improved Exp. Corn

CURRENT APPLICATION NUMBER: US/11/192,801

CURRENT FILING DATE: 2005-07-29

PRIOR APPLICATION NUMBER: US/10/232,665

PRIOR APPLICATION NUMBER: US/02-08-29

PRIOR PILING DATE: 1999-08-19

PRIOR PILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 43

SOFTWARE PatentIN Ver. 2.0

SEQ ID NO 14

LENGTH: 653
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              GTAAAAAAAGACTGTAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTAT 1545
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634 SerPheValSerAsnGluLys1leTyr1leAspLys1leGluPhe1leProVal 651
                              FRATURE:
NORME/KEY: PRT
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OTHER INFORMATION: Cry3Bb1 variant v11231
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Oy 1954 AATTATAAT- Db 594 TyrIleAsnL. Oy 1993 CAATTCCAA Db 614 ThrThrAsnS Oy 2053 GCAGATGTAT Db 634 SerPheValS	RESULT 13 US-11-192-801-16 ; Sequence 16, Applicati, ; Publication No. US2005 ; GENERAL INFORMATION: ; APPLICANT: Romano, Ch ; TITLE OF INFORMATION: ; FILE REFERENCE: 38-21	CURRENT APPLICATION N  CURRENT FILING DATE:  PRIOR PELING DATE:  PRIOR PILING DATE: 20  PRIOR APPLICATION NUM  PRIOR PILING DATE: 19  NUMBER OF SEQ ID NOS:  SOFTWARE: Patentin Ve	; SEQ ID NO 16 ; LENGTH: 653 ; TYPE: PRT ; ORGANISM: ARTIficial ; FRATURE: ; NAWE/KEY: PRT ; COCATION: (1)(653) ; OTHER INFORMATION: C	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	US-10-782-570-1 (1-2235)  QY	124	Oy 181 AATTCGAGA Db 60 A81 OY 238 GTATCCGGTA OY 298 ATAATAGGTC OY 298 ATAATAGGTC Db 85 PheAlaGlyA OY 358 GAACAAGACA
949 ATCGCTCAATTTTCTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGT 1008	CTAGATTATTTTCATTTTAGATGAACTTATATTTTATACAAA	AATAGATCTACTTATGCTACGACAGGAACTGAAATTATATATGGAAAAGAACAGGTCCA 1::	1336 CAAGTAACTCCTACTTCCCCTTTTCCTAACATATACTTTACAATTAAT 1383  135 CAAGTAACTCCTACTTCCCCCTTTTCCTAAC	GCTGGGGGGGAATTTATCTAATGATAAAAAACAACTGATTTCAATTTCCT :::	1546 AGTCATATTTATCCCAGTTTTCTTTATTTAATTATTCCTATAAAATTGGATTAGCGCTA 1605	1666 ATATCAGATAAAATAATTACAATCCAGCAATCAAAGGTAACAGTCTTGATACAAAC 1725     :::       :::     :::     :::     :::     :::     :::         :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::	1780AGTCAAGGGGGTTTAGAGATTACATGTAGAACTCCTAATTCTACACAATCTTAT 1833  548 SerAsnSerllealaLysPheLysValThrLeuAsnSerAlaAlaLeuLeuGlnArgTyr 567  1834 TACATTAGACTTCGATACGTACAAATGGTGCTGGAAATACTCTTCCTAATATATCTCTT 1893  :::   ::
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Charles P.
Improved Expression of Cry3Bb Insecticidal Protein in Plants 21(15304) Cry3Bb Improved Exp. Corn
WUMBER: US/11/192,801
: 2005-07-29
                                                             AGTACAGTAACATTACCTTTAAATCGAAACATACCATTTATATTAATCGT 2052
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LysThrMetAsnLysAspAspLeuThrTyrGlnThrPheAspLeuAla 613
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Cry3Bbl variant v11231
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424 LysValAspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAsp 443	Qy 1435 GCTGGGGGGAATTTATCTAATGATAAAAACAACTGATTTTCAATTTCCT 1485 	Qy 1486 GTAAAAAAGACTGTAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTAT 1545	1546 AGTCATATTTATCCCAGTTTTCTTTATTTAATTATTCCTATAAATTGGATTAGCGCTA	AsnTyrAlaGluCy ACAGGTGCATTAGG	493ProphepheThrTrpThrHisArgSerValAspPhePheAsnThr 507		Qy 1726 TCTAAGGTAATTGAAGGACCTGGTCATACAGGAAGCAAACTTGGTTTATTTA	Gy 1780AGTCAAGGGCGTTTAGAGATTACATGTAGAACTCCTAATTCTACACAATCTTAT 1833	1834 TACATTAGACTTCGATACGTGCTGGAAATACTCTTCCTAATATATAT	568 ArgValli:	Db 582 PheValGlnAsnSerAsnAshResearance GlnAsnSerAsnAspPheLeuValile 593	Qy         1954 AATTATAATAATTACAATACGGAGATTTTGGGTATTTC 1992           :::                      th         594 Tvr7leAanlvsThrMetAanlvsAsparaAspleuThrTvrGlnThrPheAspleuAla 613	1993	614 ThrThrAsnSerAsnMetGlyPheSerGlyAspLysAsnGluLeullelleGlyA	Qy 2053 GCAGATGTATCAATTTAATCATGATATATAATTGAATTTATACCAATT 2106 :::                   ::: Db 634 SerPheValSerAenGluLysIleTyrIleAgpLysIleGluPheIleProVal 651	RESULT 14 US-11-192-801-18 ; Sequence 18, Application US/11192801		; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants; FILE REFERENCE: 38-21(15)40 Cry3Bb Improved Exp. Corn . CIPPERM ADDIJORNTON NUMBER: 118/11/192, 8011	; CURRENT FILING DATE: 2005-07-29; PRIOR APPLICATION NUMBER: US/10/232,665; PRIOR FILING DATE: 2002-08-29	; PRIOR APPLICATION NUMBER: US/09/377,466 ; PRIOR FILING DATE: 1999-08-19 ; NUMBER OF SEQ ID NOS: 43	SEQ ID NO 18 LENGTH: 553 TYPE: DPT	ORGANISM: FEATURE:	; NAME/KEY: PRT ; LOCATION: (1)(653)
	418 CCGTTAACAGAAAGCATAAAACAGCTAAAGTTACAAACTTTAGAAGGATTTAGACAAATA 477 :::		142 PheGluaspTyrValasnalaLeuasnSerTrpLysLysLys		598 ANIGITCACAANTGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTTGAAACTGAAAACTTGAAACTTGAAACTTGAAACTGAAAACTTGAAACTTGAAACTTGAAACTTGAAACTGAAAACTTGAAAACTTGAAACTTGAAACTTGAAACTTGAAAACTTGAAAAAAAA	658 CTATTACTACTTATTATGCGCAAGCTGCTAATTTTCATTTAAATTTATTACAACAAGGT 717 	GCTGAATTGGCTGATGGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCT	214 GlnValPheGlyGluGluTrpGlyTyr22 778 GGAACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATAT 828	223SerSerGluAspValAlaGluPheTyrArgArgGlnLeuLysLeuThrGlnGlnTyr 241 829 agmaammemetaaamacommamagaagaacmaaamaamaama aga	2.2 ThrasphisCysvalAshTrpTyrasnValGlyLeuAsnGlyLeuArgGlySerThrTyr 261	ATGAGATGATATTTAATGATATCGAAGATATATGACTATTACTGTATTAGATACT	262 ABPALBITDVALLYBFDEABRAIGFREAIGATGCIORCINILGEUINIVALLEUABBLEU 201 949 ATCGCTCAATTTTCTTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGT 1008 	11eValLeuPheProPheTyrAspileArgLeuTyrSerLys	1009 OCCUPATIONANTIAN TANDAM T	1069 ACTTACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAAATTTAACACGTTCAGGG 1128	CTTAGATTATTTTCATTTTTAGATGAACTTATATTTTATACAAAA	334HIBBEGUFNEASDIYFLEUGINGIYIIEGIULNEHIBINFAKGLEUGINFFOGIYIYF 352 1174		1216 AATAGATCTACTTATGCTACGAACTGAAATTATATATGGAGAAAGAA		1336 CAAGTAACTCCCTACTTTCCCTAACATATACTTTACAATTAAT 1383		1384 CAAATTGAACTTTATTTAAATAATTCACCTAGTAATAAATTAACATATTCA 1434 ::::
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slnLeuProValValLySAlaTyrAlaLeuSerSerGly 527
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                                TATCTAATGATAAAAAAACAACTGATTTTCAATTTCCT 1485
                                                                                                            ATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTAT 1545
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|eu-----GluLysAlaTyr 473
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SerThr-----ThrAsnLeuArgLeu 581
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spAspGlnLysAsnGluThrSerThrGlnThrTyrAsp 443
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| GlnValPheGlyGluGluTrpGlyTyr----- 222
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20 GluLeuGlnThrAsnHisAsnGlnTyrProLeuAlaAspAsnProAsnSerThrLeuGlu 39
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---SerSerGluAspValAlaGluPheTyrArgArgGlnLeuLysLeuThrGlnGlnTyr 241
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| Asn------SerThrValLysAspAlaValGlyThrGlyIleSer
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207
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283
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28
                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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 Cry3Bbl variant 11231mvl
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US-11-192-801-18
                        ignment Scores:
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                                                                                ATCGCTCAATTTTTTTTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGT 1008
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|SerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGlnAspArgArgGlyThr1le---
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                       262 AspAlaTrpValLysPheAsnArgPheArgArgGluMetThrLeuThrValLeuAspLeu
                                                                                                                                                                                        389 ATGAGATGGAGTATATTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACT
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   PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnThrIleTrpProSer ---
                                                         -----AspAlaAspProTrpLysAlaPheMetAlaGlnValGluValLeuIleAspLys
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                                GAACAAGACAAAACAGTATGGACACAATTTATTAAAATGGGAGAAATTTTTGTTGATACA
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                                                                                                                                                                                                                                                                                     APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/11/192,801
CURRENT PILING DATE: 2005-07-29
PRIOR PILING DATE: 2005-07-29
PRIOR APPLICATION NUMBER: US/09/377,466
PRIOR PILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 20
LENGTH: 653
                                          1954 AATTATAAT----------AATTTACAATACGGAGATTTTGGGTATTTC 1992
                                                                                                    CAATITICCAAGTACAGTAACATTACCTTTAAATCGAAACATACCATTTATATTTAATCGT 2052
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|ThrThrAsnSerAsnMetGlyPheSerGlyAspLysAsnGluLeuIleIleGlyAlaGlu 633
64 AACAGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACCATTACAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 AACACAAATTACAAAGAGTGGCTCAATATGTGTCAA---GGGAATACACAATATGGTGAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 ATAATAGGTGCTATAATAATATTTTGGTACCCTAATCACTGTCTTTTGGCCCGCGGA 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 GTATCCGGTACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGA 297
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AsnProAsnAsnArgSerGluHisAspThr11e-----'LysValThrProAsnSer 19
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; OTHER INFORMATION: Cry3Bb1 variant 11231mv1
US-11-192-801-20
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Publication No. US20050273882A1
GENERAL INFORMATION:
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CAAATTGAACTTTATTTAAATAATTCACCTAGTAATAAATTAACATATTCA 1434 :::::::::                 LysValasppheSerGinTyrAspAspGinLysAsanGiuThrSerThrGinThrTyrasp 443	GCTGGGGGGAAITTATCIAATGAIAAAAAAACAACTGAITTTCAAITTCT 1485 	GTAAAAAAAAGACTGTAAAACCAATTATTAATCCAAATTGTFTACCAAGCTATAATAGTTAT 1545 :::    Progluthtthraspgluproleu	AGICATATITIATCCCAGITITICITIAATTAATTATTCCTATAAAATIGGATTAGGCTA 1605	AATATATATATACAGGTGCATTAGGATGGACACACAGTAGTGTTAATAGAAATAATGCA 1665 	ATATCAGATAAAATACAATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAAC 1725 	TCTAAGGTAATTGAAGGACCTGGTCATACAGGAGGAAACTTGGTTTATTACAA 1779 ::: :::	AGTCAAGGGCGTTTAGAGATTACATGTAGAACTCCTAATTCTACACAATCTTAT 1833 	TACATTAGACTTCGATACGCTACAAATGGTGCTGGAAATACTCTTCCTAATATATCTCTT 1893 	ACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAACAACATTTTTCTGGTACA 1953	AATTATAAT	CAATTICCAAGTACAGTAACATTACCTITAAATCGAAACATACCATTIATATITAATCGT 2052 	GCAGATGTATCAATTTTAATCATTGATAAATTGAATTTATACCAATT 2106 ::: SerPheValSerAanGluLyaileTyrileAspLyaileGluPheileProVal 651
1384	1435	1486	1546	1606	1666	1726 528	1780	1834	1894	1954	1993	2053
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ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGIGTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA79
TELEPHONE: 904-375-5800
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,226
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-DBV TIMEOUT=10 - WARN TIMEOUT=30 - THRRADES 1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
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Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                  -----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu
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375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn
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| GlyAspLeulle-----AspPheLyBAspHisPheLysIleThrCysGlnHisSerAsn
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524 HisSerSerValAspProLysAsnThrIleTyrThrHisLeuThrThrGlnIleProAla
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                                           GCAAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACCT----
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|112 AsnThr---TrpSerAspPhelleThrGlnThrLysAsnIleIleLysLysGluIleAla 130
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AsnThrGlnAspValArgThrGlnIleGlnLeuValHisTyrHisPheGlnAsnValIle 185
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LysPheGluAlaTyrLeuLysAsnAsnArgGlnPheAspTyrLeuGluPro---LeuPro
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                     Gaps:
INPORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1180 amino acids
TYPE: amino acid
STRANDEDNESS: aingle
TOPOLOGY: linear
MOLECULE TYPE: protein
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1153.00
54.41%
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Best Local Similarity:
Query Match:
DB:
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Percent Similarity:
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           1879 CCTAATATATCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAACAAC 1938
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                                                                                                                                                                                                                                                   602 AlaValIleAsnLeuSerIleProGlyValAlaGluLeu---GlyMetAlaLeuAsnPro
                                                                    APPLICANT:
APPLICANT:
APPLICANT: Street address: 4980 Carroll Canyon Road
APPLICANT: Citet and Diego
APPLICANT: Cate/Province: California
APPLICANT: Country: US
APPLICANT: Country: US
APPLICANT: Potenal code/Zip: 92121
APPLICANT: Poten number: (619) 453-8030 Fax number: CITLE OF INVENTION: Materials and Methods for the Control of TITLE OF INVENTION: Calliphoridae Pests
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
CITY: Galnesville
STATE: FL
                                                                                                                                                                                                                                                                                                          Sequence 28, Application PC/TUS9407902 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
ATTORNEY/CAGRAT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1180 amino acids
TYPE: amino acids
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ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TOPOLOGY: linear
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PCT-US94-07902-28
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112 AsnThr---TrpSerAspPheIleThrGlnThrLysAsnIleIleLysLysGluIleAla 130
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ValThrThrTyrLysLysGlyLeuAsnLeuIleLysThrThrProAspSerAsnLeuAsp 284
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Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                       US-10-782-570-1 (1-2235) x PCT-US94-07902-28 (1-1180)
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Patent No. 605693

GENERAL INFORMATION:
APPLICANT: Lealie Hickle
APPLICANT: Jewel Payne
TITLE OF INVENTION: Materials and Methods for the Control
TITLE OF INVENTION: Calliphoridae Pests
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: FL.
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,024
FILING DATE:
CLASSIFICATION:
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Matches:
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NAME: SAILwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA79
TELECOMMUNICATION INPORMATION:
TELEPHONE: 904-372-5800
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APPLICATION NUMBER: 08/856,226
FILING DATE:
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SEQUENCE CHARACTERISTICS:
LENGTH: 686 amino acids
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
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Best Local Similarity:
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  GATACTATCGCTCAATTTTCTTTTTTTATGATAAAGAGATACAAAGATTCAATAGGAAGA 1002
                                                                                                                                                                                                                                                                                                                                                                                                          .234 ACGACAGGAACTGAAATTATATGGGGAAAAGAACAGGTCCACCACCACAAAAACTTTA 1293
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                                                                                                       -----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu 337
                                                                                                                                                                                       ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr 374
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ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn 393
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|HisSerSerValAspProLysAsnThrIleTyrThrHisLeuThrThrGln1leProAla 543
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|564 GlyAspLeulle-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn 581
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	ThriyralaAspPheGlyfyrValThrPhePrOArgThrValProAsnLysThrPheGlu	
2010	69 CAATACGGAGATTTTTCCAATTTTCCAAGTACAGTA	19
1968 600	15 ATACCACCTCAACGACTCAACATTTTCTGGTACAAATTATAATAATTTA	19
581	 67 ThrAsnAla	, io
1914	55 ACAAATGGTGGAAATACTCTTCCTAATATTTCTCTTACAATACCAGGAGTAATAGGA	181
1854 566	98 ATTACATGTAGAACTCCTAATTCTACACAATCTTATTACATTAGACTTCGATACGCT	17.
1797	B GAAGGACCTGGTCATACAGGAGAACTTGGTTTATTTACAAAGTCAAGGGCGTTTAGAG :::	173
	509 AsnileThrGlnileH18AlaLeuLysAlaLeuLysValSerSerAspSerLysIleVal	, w
508	89 ArgvalAlaPheSerTrpThrHisThrSerValAspPheGlnAsnThrIleAspLeuAsp	
1677	18 ACAGGTGCATTAGGATGGACACACAGTGTTAATAGAAATAATGCAATATACAGATAAA	161
1617	558 TCCCAGTTTTCTTTATTTAATTATTCCTATAAAATTGGATTAGCGCTAAATATATAT	15
1557	98 TGTAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTATAGTCATAITTTA	149
1497 461	138 GGGGGGAATTTATCTAATGATAAAAACAGCTGATTTTCAATTTCCTGTAAAAAAGC 149 11	143
	23 IlelleTyrGluMetilePhePheSerAsnSerSerGluValPheArgTyrSerSer	42
422	13 GluileValArgHieArgGluTyrSerAep	
1377	18 TCAATTGTAACTGATAGACAAGTAACTCCTACTTCCCTTTTTCCTAACATATGCTTTACA	13
1317	173CCACCACAAAAAACTTTAATACCATTGAATCCTATAAAGTT 131 	12
1272 392	19 AGATCTACTTATGCTACGACAGAACTGAAATTATATATGGAGAAAGAA	12
1218 373	77 GAAACGTAC	3
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                                             TITIGCTAGIGCTGATACAATIGCTGCAGTTAGIGCAGGTACTATIGTAICCGGTACTCTG 252
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 GTATGGACACATTTATTAAAATGGGAGAAATTTTTGTTGATACACCGTTAACAGAA---
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                                                                                                                                                                                                                    APPLICANT: Country: US
APPLICANT: Postal code/Zip: 92121
APPLICANT: Phone number: (619) 453-8030 Fax number:
APPLICANT: Telex number:
TITLE OF INVENTION: Materials and Methods for the Control of TITLE OF INVENTION: Calliphoridae Pests
CORRESPONDENCE: 31
                                                                                                                                                                           4980 Carroll Canyon Road
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251
115
268
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07902
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Mismatches:
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
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Matches:
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                                                                                                                               Sequence 31, Application PC/TUS9407902 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: SAILWANCHIK, DAVIG R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA79
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-6100
TELEPAX: 904-372-5800
                                                                                                                                                                           Street address:
City: San Diego
State/Province:
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SEQUENCE CHARACTERISTICS:
LENGTH: 686 amino acids
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STATE: FL
COUNTRY: US
ZIP: 32606
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
Query Match:
DB:
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ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50C(b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-315-468-4
                            1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1318 TCAATTGTAACTGATAGACAAGTAACTCCTACTTCCCCTTTTCCTAACATATACTTTACA 1377
                                                                                                                                                                                                    ATTAATCAAATTGAACTTTATTTAAATAATTCACCTAGTAATAAATTAACATATTCAGCT 1437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      654
                                                  374 ---PheThrHisThrAsnAspAspArgAsnIleIleTrpGlyAlaValHisGlyHisIle 392
                                                                                                         393 IleSerGlnAspThrSerLysValPheProPheTyrArgAsnLysProlleAspLysVal 412
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|SefTyrlleLysThrAspAsnTyrllePheSerVal------ValArgGluArgArg 488
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567 ThrAsnAla------ProLysThrThrValPheLeuThrdlyIleAspThr 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601 ThrTyrAlaAgpPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu 620
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                                                                                                                                                                                                                                423 IlelleTyrGluMetIlePhePheSerAsnSer---SerGluValPheArgTyrSerSer 441
                                                                                                                                                                                                                                                                                                                                                     489 ArgvalalapheSerTrpThrHisThrServalAspPheGlnAsnThr11eAspLeuAsp
                                                                                   .273 ---CCACCCACAACAAAAACTTTAATACCATTTGAATCCTAT-----AAAGTT
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360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla-
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GTGAATCAAAATAATAATAATGAAATATGAGATTATCGATTCAAAGAATTTATCTTATCCT 60
APPLICANT: Michaels, Tracy Ellis
APPLICANT: Michaels, Tracy Ellis
APPLICANT: Roncerrada, Luis
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: With Bacillus thuringiensis Isolates
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: David R. Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1169
216
152
297
109
28
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
GURENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of L. Foncerrada
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/014,941
FILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 07/808,316
FILING DATE: 16-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REGISTRAPEROCO-DOCKET NUMBER: MA73.C2
TRIECOMMUNICATION INPORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: LambdaGEM-11 library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 amino acids
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787.50
47.55%
27.91%
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INDIVIDUAL ISOLATE: 50C
IMMEDIATE SOURCE:
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1 MetSerProAsnAsnGluAgnGluTyrGluIleIleAspAlaThrProSerThrSerVal 20 61 TCTAACAGAAATATTGATCATTCTACATACCTTACACAAATAATCCAAATCAACCATTA 120	58 GlySerProdiuvalPheLeuSerGluGlnAspAiavaiLysAiaAalaileAsp 75  238 GTATCGGTACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGA 297  :::	GAACAAGACAAAACAGTATGGACACAATTTATTAAAATGGGAGAAATTTTGTTGATGATACA  :::         ::		778 GGAACATCAGATGACTATTATAAAGAAAATATACCTAAATATAGTAACTAT 837 226 SeTHilleasnarTyTYTYASAACTAATAAAAGAAAATATACCTAAATATAGTAACTAT 837 226 SeTHilleasnarGaTYTYTYASAATAAGTAACTTCGAAACGAACCTAATATGATGG 838 TGTGCAAATACCTATAGAGACTAAATAACTTCGAAACGAACCTAATATGATGG 840 AGTATTTAAATGATTATCGAAGATATATGACTATTAGATACTATTGATACTATTAATGATATTAATGATATAATAATAATAATAATAATA
4 6 6 6 6 6	8 6 8 6 8		8 4 8 4 8 4 8 4	1 1 B 4 B 6 B 6 B 6 B 6

1288 ACTITA----TCAATTGTAATCCTATAAAGTT---TCAATTGTAACT 1329 1417 AATAAATTAACATATTCA---GCTGGGGGGAATTTATCTAATGATAAAAAAACAACTGAT 1473 1474 TTTCAATTTCCTGTAAAAAGACTGTAAACCAATTATTAATCCAAATTGTTTACCAAGC 1533 1951 ACAAATTATAATAATTACAATACGGAGATTTTGGGTATTTCCAATTTCCAAGTACAGTA 2010 2011 ACATTACCTTTAAATCGAAACATACCATTTATATTTAATCGTGCAGATGTATCAAATTCA 2070 2071 ATTTTAATCAFTGATAAATTGAATTTATACCAATTACTTCCTCTGTACGCCAAAATAGA 2130 CGTTCAGGGCTTAGA-----TTATTTTTCATTTTTAGATGAACTTATATTTTATACA 1170 ------TACTTTACAATTAATCAAATTGAACTTTATTTAAATAATTCACCTAGT 1416 GGATTAGCGCTAAATATATATATACAGGTGCATTAGGATGGACACACAGTAGTGTTAAT 1653 1654 AGAAATAATGCAATATCAGATAAATAATTACAATGATCCCAGCAATCAAAGGTAACAGT 1713 1714 CTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAGGAAACTTGGTTTAT 1773 TTACAAAGTCAA---GGGCGTTTAGAGATTACATGTAGAACTCCTAATTCTACACAATCT 1830 CTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAACAACACTTTTTCTGGT 1950 354 LystysArgSerPhcThrSerAspArgTyrMetArgTyrTrpAlaGlyHisGln1leSer 373 374 TyrLysHisIleGlyThrSerSerThrPheThrGlnMetTyrGly-----ThrAsnGln 391 392 AgnLeuGlnSerThrSerAgnPheAgpPheThrAgnTyrAgpIleTyrLygThrLeuSer 411 iii 412 AsnGlyAlaValLeuLeuAspIleValTyrProGlyTyrThrTyrThrPhePheGlyMet 431 r::||| :::||| :::||||:::
ProGluThrGluPhePheMetValAsnGlnLeu-------AsnAsnThrArg 446 512 :::::: |||||| | ::: |||||| | SerValAsnAlaSerSerAsnIleGlnArdsnThrAsn 645 ----SerSerThrSerThrTyrValProValPheSerTrpThrHisArgSerAlaAsp AAAAATGAAACGTAC---GGGAATCGTTTAGTTGGTATTGCGAATCGTAATAGATCTACT 1330 GATAGACAAGTAACTCCTACTTCCCTTTTCCTAACATA------1774 1534 1891 1171 1228 1369 447 495 646

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ATCGCTCAATTTTTTTTTTTATCATATAAGAGATACAAAGATTCAATAGGAAGAATAGGT 1008
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84 PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnAlaIleTrpProSer--- 102
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154 ---AlaproValAsnLeuArgSerArgArgSerGlnAspArgIleArgGluLeuPheSer 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        598 AATGITCACAATGATTITTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAAACG 657
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                                                                                                                                                                                                                                                                118 TTACAAAACACAAATTACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGT 177
                                                                                                                                                                                                                                                                                                                                      178 GATAATITICGAGACATITIGCIAGIGCIGATACAATIGCIGCAGITAGIGCAGGIACIAIT 237
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21 ProThrAsn------HisAsnGlnTyrProLeuAlaAspAsnProAsnSerThr
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1 MetAsnProAsnAsnAsnAsgSerGluTyrAspThrIleLysValThrProAsnSerGluLeu
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37 LeuGluGluLeuAsnTyrLysGluPheLeuArgMetThralaAspAsnSerThr----
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213 GlnValPheGlyGluGluTrpGlyTyr-------
        116
270
148
31
   Conservative:
Mismatches:
Indels:
Gaps:
                                                                                           US-10-782-570-1 (1-2235) x US-08-315-468-6 (1-651)
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28.80%
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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        681
                                APPLICANT: Michaels, Tracy Ellis
APPLICANT: Michaels, Luis
APPLICANT: Marva, Kenneth E.
TITLE OF INVENTION: Process for Controlling Scarab Pests
TITLE OF INVENTION: With Bacillus thuringiensis Isolates
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER: ERADABLE FORM:
MEDIUM TYPE: PLOCOMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Bacharin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/315,468
                                                                             2191 AAAAATACTTTAAATATAGAAGCCACAAACTATGATATTGAT 2232
                                                                                               651
216
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IMMEDIATE SOURCE:
CLONE: E. coli XLI-Blue (pM1,98-4), NRRL B-18291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIPICATION: 424
PRICEATION HOATA:
APPLICATION NUMBER: US/08/014,941
PILING DATE: 07/828,430
PILING DATE: 30-JAN-1992
PRICEATION NUMBER: 07/828,430
PILING DATE: 30-JAN-1992
PRICEATION NUMBER: 07/808,316
APPLICATION NUMBER: 15-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REGISCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus thuringiensis
                                                                                                                                                                               Sequence 6, Application US/08315468
Patent No. 5554534
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 651 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , LOCATION:
US-08-315-468-6
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Pred. No.:
                                                                                                                                                                   -08-315-468-6
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FEATURE:
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QY         1987 TATTTCCAATTTCCAAGTACAGTAACATTACCTTTAAATCGAAACATACCATTT         2040           Db         606 TyrGlnThrPheAspPheAlaThrSerAsnSerAsnMetGlyPhe 620           QY         2041 ATATTTAATCGTGCAGAT	Sequence 4, Application US/07941650A Patent No. 6.2541L REMEMA: INCOMATION: APPLICANT: Braditach, Gregory A. ITITIE OF INVENTION: COUNTRY: OF INVENTION: Process for Controlling Lepidopteran Pests CORRESPONDENCE: Saliwanchik STREST: ALS ADDRESS: CORRESPONDENCE: Saliwanchik STREST: ALS ADDRESS: COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: TIMP POCOMPATION COUNTRY: TIMP POCOMPATI	#WOLECULE TYES #WOLECULE TYES ANTI-SENSE: NO RIGINAL SOURCE: CRGANISM: Bacillus thuringiensis FTRAIN: tolworth: FINDIALY SOURCE: CLONE: B. coli XLI-Blue (pMI,98-4), NRRL B-18291 FRAINE: NAME/KEY: Protein LOCATION: 1.651 US-07-941-650A-4
IleValLeuPheProPheTyrAspValArgLeuTyrSerLys		

	TCAAAGAATTTATCTTAT 57	8 H	ATACACAATATGGT 177   ::: snSerThr 54	JTGCAGGTACTATT 237      YThrGlylleSer 71	CCGGACCGATAGGA 297 ::: Valpro 83		FTTTGTTGATACA 417 :: :::    alleulleAspLys 120	AATTTAGACAAATA 477    	GACTACAAGCTCCT 537	AAATACGATTTGAG 597 :: rgGluLeuPheSer 172	AAACTIATAAAACG 657 :::::: erLygPheGluVal 192	TATTACAACAAGGT 717       :: euLeulysAspala 212	TTGAACCTAATGCT 777	ATATACCTAAATAT 828 :::    euThrGlnGlnTyr 240	GAAACGAACCTAAT 888 	
Length: 651 Matches: 216 Conservative: 116 Mismatches: 270 Indels: 148 Gaps: 31	۱ >	CCTTCTAACAGAAATATTGATGATTCTAGATACCCTTACACAAATAATCCAAATCAACCA	TTACAAAACACAAATTACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGT    :::     :::             -:::     -euGluGluGluLeuAsnfyrLysGluPheLeuArgMetThralaAspAsnSerThr	GATAATTTCGAGACATTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATT 	GTATCCGGTACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGA	ATAATAGGTGCTATAATAATATCTTTTGGTACCCTAATCACTGTCTTTTGGCCCGGGA         ::: 	GAACAAGACAAAACAGTATGGACACAATTTATTAAAATGGGGAAAATTTTTGTTGATACA 	CCGTTAACAGAAAGCATAAAACAGCTAAAGTTACAAACTTTAGAAGGATTTAGACAAATA 	TTACAAAGCTATAATACAGCATTAGATGATGAAAAAATTAAAAAGACTACAAGCTCCT ::	GGATTACCACCATCATCAGCATTACAACAAGCTGCCTTGACTTAAAATACGATTTGAG 	AATGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAACG	CTATTACTACTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATACAACAGGT 	GCTGAATTGGCTGATGAATGGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCT 	ACATCAGATGACTATTATAAACTTTTAAAAGAAAATATATACCTAAATAT :::   ::    SerSerGluAspIleAlaGluPheTyrGlnArgGlnLeuLysLeuThrGlnGlnTyr	agtaactattgtgcaaatacctatagagagactaaaataaacttgaaaggacctaat :::::::	<b>ЪТ</b> КЗВ БЪТ В ТЕТЕТ В ТЕ
es: 1.37e-55 706.00 rity: 44.27% ilarity: 28.80%	(1-2235) x US-07-941-650A-4 (1-651)   GTGAATCAAATAATAATGAATATGAGATTATCGAT	CCTTCTAACAGAAATATTGAT	TTACAAACACAAATTACAAA     :::  -                        LeuGluGluLeuAenTyrLye	GATAATTTCGAGACATTTGCT     ;GluValLeuagp	GTATCCGGTACTCTGTTAGCCGGTATAGGT 	ATAATAGGTGCTATAATAATA         PheAlaGlyAlaLeuThrSer	GAACAAGACAAAACAGTATGG      AspalaaspProTrp	CCGTTAACAGAAAGCATAAAA ::: LysileGluGluTyralalyb	TTACAAAGCTATAATACAGCATTAGATGAGAAAAT :::	GGATTACCACCATCATCAGCA      ::: AlaProValAsnLeuArg	AATGTTCACAATGATTTTATT :::     GlnalaGluSerHiBPheArg	CTAFTACTACCTATTTATGCG	GCTGAATTGGCTGATGAATGGAATGCAGAT.::	GGAACATCAGATGAC :::   ::    SerSerGluAspIleAls	AGTAACTATTGTGCAAATACC	E & WILLIAM CHANGE A COMMAND & COMMA
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similari Db:	US-10-782-570- Qy 1	58 21	Qy 118 Db 37	Qy 178 of Db 55	Qy 238	Oy 298	Oy 358 Db 103	Oy 418 Db 121	Qy 478 Db 141	Oy 538 Db 154	Oy 598 Db 173	Qy 658 Db 193	Oy 718	Oy 778 Db 222	Oy 829 Db 241	

1008	1068 313	1128 332	1173 351	1215 368	1275 388	1335	1383	1434	1464	1524 470	1584 485	1644	1704	1764 539	1812 559	1872 575	1932 585
94	13	AGGG 112:	351	STATTGCGAATCGT 121 ::: ValGluThrArg 368	127 388	CTTTAATACCATTTGAATCCTATAAGTTTCAATTGTAACTGATAGA 133	138	rtraaataattcacctagraataaattaAcatattca 143:	ATAAAAAA 146   ::: BpGlnLeuProProGlu 462	TCCTGTAAAAAGACTGTAAACCAATTATTAATCCAAATTGT 15    ::::::    uProleuglulyb47	ATAGTCATATTTATCCCAGTTTTCTTTATTTAATTATTC 158                ::: yrSerHisGlnLeuAsnTyrAlaGluCy8PheLeuMetGln 485	164	170 519	176 539	AGTCAAGGGGTTTAGACATTACATGTAGAACT 181	187 575	193 585
ATCGCTCAAT	GCATTAAA!   :::     :lyVallys1	CTTACCTTC	TTAGATTAT	SerGlyLysAspS	ATAGATCT? Proserile(	CCCACAACAA         ProlleGlm	CAAGTA ::: ThrileAla	AAATTGAA( ::::::::: :ysvalaspl	GCT ::: SerLysArg1	ACAACTGAT	TTACCAAGC	FATAAAATTO ::: ABDArgArgo	AGTGTTAAT/       ::: Servalaspi	GTAACAGTO ::: AlaTyrAlal	TTGGTTTATTTACAA    :::::   :: LeuLeuPheLeuLygG]	ccraarrcr. AlaalaLeu)	ACTCTTCCT.
949 A 281 I	1009 G	1069 A	333 -	1174 - 352 S	1216 A 369 F	1276 C	1336 0	1384 C : 423 I	1435 G 443 S	1465 A 463 T	1525 7	1585 7	1645 7	1705 (	1765 7 540 I	1813 (	1873 7

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949 ATCGCTCAATTTTCTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGT 1008
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92 PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnAlaIleTrpProSer--- 110
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                                                               CCTTCTAACAGAAATATTGATCTAGATACCCTTACACAAATAATCCAAATCAACCA 117
                                                                                                                              118 TTACAAAACACAAATTACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGT 177
                                                                                                                                                                                                                                                             GTATCCGGTACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGA 297
                                                                                                                                                                                                                                                                                                                            298 ATAATAGGTGCTATAATAATATCTTTTGGTACCCTAATCACTGTCTTTTGGCCCGCGGGA 357
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                                                                                                                                                -----GluValLeuAspSerSerThrValLysAspAlaValGlyThrGlyIleSer 79
                                                                                                                                                                                                                                                                                GTGAATCAAAATAATAATAATGAATATGAGATTATCGAT----TCAAAGAATTTATCTTAT
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MetAsnProAsnAsnArgSerGluTyrAspThrIleLysValThrProAsnSerGluLeu
                                                                                    29 ProThrasn-------HisasnGlnTyrProLeualaaaspanProAsnSerThr
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AACAACACTTTTTCTGGTACAAATTATAATAATTTACAATAC-----GGAGATTTTGGG 1986
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------ABNSerABNMetGlyPhe 620
                                                                                                                                                          621 SerGlyAspThrAsnAspPhellelleGlyAlaGluSerPheValSerAsnGluLyslle 640
                            AsnAsnAspPheLeuVallleTyrIleAsnLysThrMetAsnIleAspGlyAspLeuThr 605
                                                              TAT-----TICCAATITICCAAGTACAGTACATTACCTTTAAATCGAAACATACCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INSECT-RESISTANT TRANSGENIC PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,441B
FILING DATE: 18-DEC-1997
ATTOMER: ALCCHIN: 800
ATTOMER/AGENT INPORMATION:
NAME: KAtchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
TELEPHONE: 512/418-3000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE GIARACTERISTICS:
LENGTH: 659 amino acids
TENGTH: 659 amino acids
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116
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                            2077 ATCATTGATAAATTGAATTTATACCAATT 2106
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                                                                                                                            1041 ATATTTAATCGTGCAGAT------
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CITY: Houston STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Tersch, Michael A.
APPLICANT: Romano, Charles
TITLE OF INVENTION: INSECT-RESISTANT
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                        Sequence 112, Application US/08996441B
Patent No. 6023013
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       English, Leigh H.
Brussock, Susan M.
Malvar, Thomas M.
Bryson, James W.
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44.27%
28.80%
17.92%
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Query Match:
DB:
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629 SerGlyAspThrAsnAspPheIleIleGlyAlaGluSerPheValSerAsnGluLysIle 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGAATCAAAATAATAATAATGAATATGAGATTATCGAT---TCAAAGAATTTATCTTAT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INPORMATION:
APPLICANT: Brussock, Susan M.
APPLICANT: Brussock, Susan M.
APPLICANT: Brussock, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Malters, Frederick S.
APPLICANT: Walters, Frederick S.
APPLICANT: Won Terech, Michael A.
APPLICANT: Romano, Charles
TITLE OF INVENTION: NUCLEIC ACID SEGMENTS ENCODING MODIFIED
TITLE OF INVENTION: OLEOPTERAN-TOXIC CRYSTAL PROTEINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDORS Milte & Durkee
STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             659
216
116
270
270
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COMPUTER: IBM PC compatible
ODFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLION NUMBER: US/08/993,722A
FILLIO DATE: 18-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                2077 ATCATTGATAAATTGAATTTATACCAATT 2106
                                             FILING DATE: 18-DBC-199,
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:149
TELECOMMINICATION INFORMATION:
TELEPHONE: 512/418-3106
TELEFAX: 512/474-7577
                                                                                                                     ; Sequence 112, Application US/08993722A ; Patent No. 6060594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRIEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
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706.00
44.27%
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MEDIUM TYPE: Floppy
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US-08-993-722A-112
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451 SerLysArgTyrAsnGlyTyrLeuGlyAlaGlnAspSerIleAspGlnLeuProProGlu 470
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568 AlaAlaLeuLeuGlnArgTyrArgValArgIleArgTyrAlaSerThr-------
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                                                 CTTAGATTATTTTCATTTTAGATGAACTTATATTTTTATACAAAA-----
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	62 237 79 297 357	110 417 128 477	### ##################################	GlnAlaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPheGluVal 200  CTATTACTACTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATTACAACAAGGT 717  [I	248 888 268 948	AspalatrpvallysPheAsnargPheArgArgGluMerThrLeuThrValleuAspleu 288  ATCGCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGAATAGGT 1008	ACTTACCTGAAATTCAACCCAATCTCGCTAIAATGGAATATTAACACGTTCAGGG 1128 AlaLeuGlndlufyrGlyProThrPheSerSerIeGludanSerIleArgyPero 340 CTTAGATTATTTTTATAGATGAACTTATATTTTATACAAA

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1174 -------AATGAAACGTACGGAATCGTTTAGTTGCTATTGCGAATCGT 1215
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                                          198 ATAATAGGTGCTATAATAATATCTTTTGGTACCCTAATCACTGTCTTTTGGCCCGCGGGA 357
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230 ---SerSerGluAspIleAlaGluPheTyrGlnArgGlnLeuLysLeuThrGlnGlnTyr
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                                                                                                               149 PheGluappTyrValasnalaLeuAspSerTrpLysLysLys
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|LeuGluLeuABnTyrLysGluPheLeuArgMetThrAlaAspAsnSerThr----- 62
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------GluValLeuAspSerThrValLysAspAlaValGlyThrGlyIleSer
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: English, Leigh H.
APPLICANT: Brussock, Susan M.
APPLICANT: Brussock, Susan M.
APPLICANT: Brussock, James M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Malvar, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Malvers, Prederick S.
APPLICANT: Statin, Stephen L.
TITLE OF INVENTION: POLYPEPTIDE COMPOSITIONS TOXIC TO TITLE OF INVENTION: COLEOPTERAN INSECTS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STRATE: Texas
COUNTRY: USA
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MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPARING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,170A
FILING DATE: 18-DEC-1997
CLASSITCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/OPCKET NUMBER: 33,928
REFERENCE/OPCKET NUMBER: 33,928
TELERPMONICATION INFORMATION:
TELERPMONICATION INFORMATION:
TELERPMONICATION INFORMATION:
TELERPMONICATION INFORMATION:
TELERPMONICATION SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
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Matches:
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Best Local Similarity:
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92 PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnAlaIleTrpProSer--- 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METHODS FOR IMPROVING THE ACTIVITY OF DELTA-ENDOTOXINS AGAINST INSECT PESTS
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,775B
FILING DATE: 18-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: MECO:150
TELERPHONE: 512/418-3000
TELERPHONE: 512/418-3000
TELERPHONE: 512/418-3000
TELERPHONE: 512/418-3000
TELERPHONE: 512/418-3000
TELERPHONE: SI2/414-7577
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
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116
270
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                  ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
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706.00
44.27%
28.80%
17.92%
TITLE OF INVENTION: DEI TITLE OF INVENTION: DEI NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
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US-08-993-775B-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity:
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1336 CAAGTA-----ACTCCTACTTCCCCTTTTCCTAAC-----ATATACTTTACAATTAAT 1383
                                                                    CAAATTGAACTTTATTTAAATAATTCACCTAGTAATAAATTA------ACATATTCA 1434
                                                                                                                                       GCT------AAA 1464
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                     451 SerLysArgTyrAsnGlyTyrLeuGlyAlaGlnAspSerIleAspGlnLeuProProGlu 470
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479 -------AlaTyrSerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGln 493
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LysValAspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAsp
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568 AlaAlaLeuLeuGlnArgTyrArgValArgIleArgTyrAlaSerThr------
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APPLICANT: BRUSBOCK, SUSAN M.
APPLICANT: MALVAR, Thomas M.
APPLICANT: MALVAR, Thomas M.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Prederick S.
APPLICANT: Statin, Stephen L.
APPLICANT: Statin, Stephen L.
APPLICANT: Von Tersch, Michael A.
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451	1525	1585	Qy 1645 ACTGTTAATAGAATAATGCAATATCGGTAAAA       :::              ::: 	1705 GGTAACAGTCTTGATACAAACTCTAA :::    ::: :: 528 AlaTyrAlaLeuSerSerGlyAlaSe	1765	568	18/3 584	1933 AACAAC          594 AsnAsn	1987	2041 ATATTTAATCGTGGAAT	Cy 2077 ATCATTGATAAATTGATTTATACCAATT 210  Db 649 TyrileAspLysileGluPheileProVal 656	RESULT 12 US-09-427-770-112 ; Sequence 112, Application US/09427770 ; Patent No. 6620988	; GENEKAL INVOKWATION: ; APPLICANT: English, Leigh H. ; APPLICANT: Brussock, Susan M. ; APPLICANT: Malvar, Thomas M.	APPLICANT: Bryson, James W. APPLICANT: Kulesza, Caroline A. APPLICANT: Walters, Frederick S. APPLICANT: Slatin, Stephen L.	APPLICANT: Von Tersch, Michael A. APPLICANT: Romano, Charles ITILE OF INVENTION: WCLEIC ACID SEGMENTS ITILE OF INVENTION: COLEOPTERAN-TOXIC CRYS	ONDENCES: ONDENCE ADDRESS SSEE: Arnold, T: P.O. Box 44	; STATE: TOWNED: ; STATE: Texas ; COUNTRY: USA
	538 GGATTACCACCATCACAGCATTACAAGAGCTGCCTTGACTCTTAAAATACGATTTGAG 597     :: :        ::          162    178    162    162    163    164    164    165    160	598 AATGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAAACG 657 ::::	658 CTATTACTACTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATTACAACAAGGT 717 	Gaatgcagatatacatccttcacaaaittgaacctaatgct   pglytyr	778 GGAACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATAT 828 :::   :::    :::	829 AGTAACTATTGTGCAAATACCTATAGAGAAGACTAAATAAA	889 ATGAGAGGAGTATATTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACT 948 	949 ATCGCTCAATTTTCTTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGT 1008 	1009 GGCATTAAAACTGAACTTACAAGAGAAATTTATACAACTGAAATAAAT	1069 ACTTACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAATTTAACACGTTCAGGG 1128 122 AlaLeuGlnGlutyrGlyProThrPheSerSerIleGluAenSerIleArgLyBro 340	1129 CTTAGATTATTTTCATTTTTTAGATGAACTTATATTTTATACAAAA	1174AATGAAACGTACGGAATCGTTTAGTTGGTATTGCGAATCGT 1215	1216 AATAGATCTACTACGACAGGAACTGAAATTATATATGGAGAAAGAA	1276 CCCACAAAAAATTTTAATACCATTTGAATCCTATAAAGTTTCAATTGTAACTGATAGA 1335 	1336 CAAGTAACTCCTACTTCCCCTTTTCCTAACATATACTTTACAATTAAT 1383 11	1384 CAAATTGAACTTTATTTAAATACTCACCTAGTAATAAATTAACATATTCA 1434 :::::::::	1435 GCT
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TCGATACGCTACAAATGGTGCTGGAAAT 1872 :||||||||||:: eArgTyrAlaSerThr-----583 ATTACCTTTAAATCGAAACATACCATTT 2040 TGAAGGACCTGGTCATACAGGAGGAAAC 1764 AGGGCGTTTAGAGATTACATGTAGAACT 1812
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eAlaLysPheLysValThrLeuAsnSer 567 AGTAATAGGAATACCACCTCAACGACTC 1932 ------GIAICAAAITCAAITTTA 2076 |||||||| aGluSerPheValSerAsnGluLysIle 648 ATCCCAGTTTTCTTTATTTATTTCC 1584 TTTACAATAC-----GGAGATTTTGGG 1986 CTGTAAACCAATTATTAATCCAAATTGT 1524 |::: uAsnTyrAlaGluCysPheLeuMetGln 493 -----GlnAsnSer 593 |||||| |SThrMetAsnIleAspGlyAspLeuThr 613 nAspSerIleAspGlnLeuProProGlu 470 S ENCODING MODIFIED YSTAL PROTEINS 106

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-------AATGAAACGTACGCAATCGTTTAGTTGGTATTGCGAATCGT 1215
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---HisLeuPheAapTyrLeuArgGlyIleGluPheHisThrArgLeuArgProGlyTyr 359
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                                           ||| ::: |||| ::: :---AlaProValAsnLeuArgSerArgArgSerGlnAspArgIleArgGluLeuPheSer
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---SerSerGluAspileAlaGluPheTyrGlnArgGlnLeuLysLeuThrGlnGlnTyr
          GGATTACCACCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAG
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|PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnAlaIleTrpProSer--- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::: ||| :::
LysIleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAsnAsn 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAACAAGACAAAACAGTATGGACACAATTTATAAAATGGGAGAAATTTTGTTGATACA 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTTCTAACAGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACCA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATAATTTCGAGACATTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATT 237
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ProThrAsn------HisAsnGlnTyrProLeuAlaAspAsnProAsnSerThr 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GiuValLeuAspSerSerThrValLysAspAlaVaiGlyThrGlyIleSer 79
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|FeuGluGluLeuAsnTyrLysGluPheLeuArgMetThrAlaAspAsnSerThr----
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216
1116
270
31
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/427,770
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/993,722
FILING DATE: 18-DEC-1997
ATTONEY/ACBVI TINFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: 33,928
REFERENCE/DOCKET NUMBER: 33,928
TELEPHONE: 512/418-3106
TELEPHONE: 512/418-3106
TELEPARATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
CLOSE OF THE COLUMBER: 1200 DELEPARATION POR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
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706.00
44.27%
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TYPE: amino acid
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 ATAATAGGTGCTATAATAATATCTTTTGGTACCCTAATCACTGTCTTTTTGGCCCGCGGGA 357
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45 LeuGluGluLeuAsnTyrLysGluPheLeuArgMetThrAlaAspAsnSerThr----
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/427,769
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,722
FILING DATE:
ATTORNEY/AGRAT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:149
TELEPHONE: 512/418-3106
                                                                                                                                                                                                                                          TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
TYPE: amino acid
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706.00
44.27%
28.80%
17.92%
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                                                                                                                                                                                                                              GGTAACAGTCTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAGGAAAC 1764
                                                                                                                                                                                                                                                                                                         TTGGTTTATTTACAA------AGTCAAGGGCGTTTAGAGATTACATGTAGAACT 1812
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         AGTGTTAATAGAAATAATGCAATATCAGATAAAATAATTACAATGATCCCAGCAATCAAA 1704
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-----ThrAsnLeuArgLeuPheVal-------GlnAsnSer 593
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                                                                                                                                                                            594 AsnAsnAspPheLeuValIleTyrIleAsnLysThrMetAsnIleAspGlyAspLeuThr 613
                                            ------AlaTyrSerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGln 493
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LeuLeuPheLeuLysGluSerSerAsnSerIleAlaLysPheLysValThrLeuAsnSer
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Patent No. 6642030

GENERAL INFORMATION:

APPLICANT: Brussock, Susan M.

APPLICANT: Brussock, Susan M.

APPLICANT: Brussock, Susan M.

APPLICANT: Brussock, Susan M.

APPLICANT: Walters, Frederick S.

APPLICANT: Walters, Frederick S.

APPLICANT: Slatin, Stephen L.

APPLICANT: Somano, Charles

TITLE OF INVENTION: OUGLEOPTERAN-TOXIC CRYSTAL PROTEINS

WANTHIN OF INVENTION: CLEOPTERAN-TOXIC CRYSTAL PROTEINS
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CORRESSONDENCE ADDRESS:
ALTOIG, White & Durkee
STREET: P.O. Box 4433
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOPTWARE: Patentin Release #1.0,
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STATE: Texas
COUNTRY: USA
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	249 ThrAspHisCysValAsnTrpTyrAsnValGlyLeuAsnSerLeuArgGlySerThrTyr 268  889 ATGAGATGAGATATTTAATGATTATCGAAGATATACTGTATTAGATATTAGATATTAGATATTAGATATTAGATATTAGATATTAGATATTAGATATTAGATATTAGATATTAGATATTAGATATTAGATATAGATATTAGATATTAGATATAGATATAGATATAGATAGAAGA		GCT
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/sPheLysValThrLeuAsnSer 567
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|ProGlyPheThrGlyGlyAen 547
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/rAlaSerThr-----583
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stasnileaspGlyAspLeuthr 613
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                      TACAATGATCCCAGCAATCAAA 1704
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-----TrpThrHisArg 507
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|LeuGluGluLeuAgnTyrLygGluPheLeuArgMetThrGluAgpSerSerThrGluVal
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ProThrAsn------HisAsnGlnTyrProLeuAlaAspAsnProAsnSerThr
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70 IleSerValValGlyGlnIleLeuGlyValValGly-------
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|Ser-----AspalaAspProTrpLysAlaPheMetAlaGlnValGluValLeuIle
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Matches:
Conservative:
Mismatches:
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     MECO:151
REFERENCE/DOCKET NUMBER: MECO:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-7577
SROUGHOS CHARACTERISTICS:
LENGTH: 652 animo acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-996-441B-110
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700.00
44.58%
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Query Match:
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                         333 HisLeuPheAspTyrLeuGlnGly1leGluPheHisThrArgLeuGlnProGlyTyrSer
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464 Thrasp-----GluproLeuGluLys-----
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|LeuGluGluLeuAsnTyrLysGluPheLeuArgMetThrGluAspSerSerThrGluVal 56
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| 139 AsnAsnPheGluAspTyrValAsnAlaLeuAsnSerTrpLysLys
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216
1117
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142
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                           4.82e-55
700.00
44.58%
28.92%
17.77%
   ; TOPOLOGY: linear
US-08-993-722A-110
                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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GITTATTTACAA------AGTCAAGGCGTTTAGAGATTACATGTAGAACTCCT 1815
                                                                                                                  1816 AATTCTACAATCTTATTACATTAGACTTCGATACGCTACAAATGGTGCTGGAAATACT 1875
                                                                                                                                                                                                                                       1876 CTTCCTAATATATCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAAC 1935
                                                                                                                                                                                                                                                                                                                                                         AACACTTTTTCTGGTACAAATTATAATAATTTACAATAC-----GGAGATTTTGGGTAT 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .990 TTCCAATTTCCAAGTACAGTAACATTACCTTTAAATCGAAACATACCATTT----- 2040
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                                 576 ---ThrashLeuargLeuPheVal--------GlnasnSerash 586
                                                                                                                                                                                                                                                                                                                                                                                                             587 AsnAspaheileValileTyrileAsnLysThrMetAsnIleAspAspAspAspLeuThrTyr 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                561 AlaLeuLeuGlnArgTyrArgValArgIleArgTyrAlaSerThr-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brissork, Susan M.
APPLICANT: Brissork, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Brissor, James W.
APPLICANT: Statin, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Statin, Stephen L.
APPLICANT: Statin, Michael A.
APPLICANT: Nomano, Charles
TITLE OF INVENTION: NUCLETC ACID SEGMENTS ENCODING MODIFIED
TITLE OF INVENTION: COLEOPTERAN-TOXIC CRYSTAL PROTEINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,722A
FILING DATE: 18-DEC-1997
CLASSIP ICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REPRENCY/COCKET NUMBER: MECO:149
TELEPHONE: 512/418-3106
TELEPHONE: 512/418-4757
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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US-08-993-722A-110
; Sequence 110, Application US/08993722A
; Patent No. 606094
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T: Brussock, Susan M.
T: Malvar, Thomas M.
T: Bryson, James W.
T: Kulesza, Caroline A.
T: Walters, Frederick S.
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& <del>8</del>	892 AG 262 Al	AGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACTATC 951 
È	952 GC	GCTCAATITTCTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGC 1011 
Д		
දු ද	1012 AT :: 296 Va	ATTAAAACTGAACTTACAAGAGAAATTTATACAACTGAAATAAAT
È	1072 TA	CCTTGAAAITCAACCCAATCTCGCTATAATGGAATATAATTTAACACGTTCAGGGCTT 1131
DP DP	315 Le	LeuGlnGluTyrGlyProThrPheLeuSerIleGluAsnSerIleArgLysPro 332
ò	1132 AG	AGATTATTTTTAGATGAACTTATATTTTTATACAAA
Db	333 Hi	sLeuPheAspTyrLeuGlnGly1leGluPheHisThrArgLeuGlnProGlyTyrSer 352
ò	1174	
ΩP	353 GI	yLysAspSerPheAsnTyrTrpSerGlyAsnTyrValGluThrArgPro 369
ò	1219 AG	AGAICTACTIAIGCTACGACAGGAACTGAAATTATATGGAGAAAGAAGGACGGCCCC 1278
gg	370 Se	rlleGlySerSerLysThrileThrSerProPheTyrdlyAspLysSerThrGluPro 389
È	1279 AC	ACAACAAAAACTITAATACCATTTGAATCCTATAAAGTITCAATTGTAACTGATAGACAA 1338
g G	390 Va	lGlnLysLeuSerPheAspGlyGlnLysValTyrArgThr 403
È		GIAACTCCTACTTCCCTATTTCCTAACADATACATTAATCAA 1386
<b>Q</b>	404 Il	eAlaAsnThrAspValAlaAlaTrpProAsnGlyLysIleTyrPheGlyValThrLys 423.
È		ATTGAACTTTATTTAAATAATTCACCTAGTAATAAATTAACATATTCAGCT 1437
ପୁ	424 Va	
ò	1438	
Q	444 Ly	sArgAsnAsnGlyHisValdlyAlaGlnAspSerileAspGlnLeuProProGluThr 463
È	1468 AC	ACTGATTTTCAATTTCCTGTAAAAAAAGACTGTAAACCAATTATTAATCCAAATTGTTTA 1527
qq	464 Th	  riaspGlubroLeuGluLys
È	1528 CC	CCAAGCTATAATAGTTATAGTCATATTTTATCCCAGTTTTCTTTAATTAA
Db	471	AlaTyrSerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGlnAsp 486
È	1588 AA	AAAAITGGAITAGCGCTAAAITATATTATACAGGTGCATTAGGATGGACACACAGTAGT 1647
qα	487 Ar	gargdlyThrIleProPhePheThrTrpThrHiBargSer 500
È	1648 GT	GITAATAGAAATAATGCAATATCAGATAAAATAAATGATGATCCCAGCAATCAAAGGT 1707
qq	501 Va	ilaspPhePheAsnThrIleAspAlaGluLysIleThrGlnLeuProValVallysAla 520
ò	1708 AA	ACAGTCTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAGGAAACTTG 1767
qq	521 Ty	TyralaLeuSerSerGlyalaSerIleIleGluGlyProGlyPheThrGlyGlyAsnLeu 540
È	1768 G7	GITTATITIACAAAGICAAGGCGTITIAGAGAITIACAIGTAGAACICCT 1815
q	541 Le	LeupheleulysGluSerSerAsnSerIleAlaLysPhelysValThrLeuAsnSerAla 560
È	1816 A	AATTCTACACATTTATTACATTAGACTTCGATACGCTACAAATGGTGCTGGAATACT 1875
Dp	561 A]	
ò	1876 CT	1876 CTTCCTAATATATCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAAC 1935

586	1989	909	2040	623	2085	643		
:::         576ThrAsnLeuArgLeuPheValGlnAsnSerAsn 586	1936 AACACTTTTTCTGGTACAAATTATAATAATTTACAATACGGAGATTTTGGGTAT 1989	   S87 AsnAspPhelleVallleTyrIleAsnLysThrMetAsnIleAspAspAspLeuThrTyr 606	1990 TICCAATTICCAAGIACAGTAACATTACCTTIAAAICGAAACAIACCAITT 2040	607 GlnThrPheAspLeuAlaThrThrAsnSerAsnMetGlyPheSerGlyAsp 623	1ATAITIAATCGIGCAGAIGIATCAAATICAAAITITAAICAIIGAI 2085	524 ThrAsnGluLeullelleGlyAlaGluSerPheValSerAsnGluLyslleTyrlleAsp 643	2086 AAAATTGAATTTATACCAATT 2106	
576	193(	58,	199	.09	2041	62,	208	64
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Search completed: January 12, 2006, 06:41:17 Job time : 88 secs

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